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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:18:25 ; Search time 50 seconds
(without alignments)
4584.774 Million cell updates/sec

Title: US-09-873-409-2
Perfect score: 4079
Sequence: 1 MVDENDIRALNVHRDHIG.....QELLNRDIYFKLVNAQSVQ 812

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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3	4079	100.0	1195	US-09-873-409-6
4	4079	100.0	1222	US-09-873-409-5
5	3919	96.1	1232	US-10-415-378-14
6	3323	81.5	659	US-09-873-409-1
7	3188.5	77.7	1354	US-10-092-900A-304
8	2465.5	60.4	1066	US-09-817-762-5
9	2465.5	60.4	1275	US-10-363-112-49
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13	2441	59.8	1272	US-09-769-097-2
14	2441	59.8	1272	US-09-769-097-4
15	2441	59.8	1280	US-10-101-433A-3

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Sequence 7, Appli	23	2438	59.8	1280	16	US-10-619-359A-7
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Sequence 3, Appli	38	2436	59.7	1280	16	US-10-343-657-4
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ALIGNMENTS

RESULT 1
US-09-873-409-2
; Sequence 2, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-873-409-2

Query Match	100.0%;	Score 4079;	DB 9;	Length 812;
Best Local Similarity	100.0%;	Pred. No. 0;		
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			Indels	0;
			Gaps	0;
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Db	1	MVDENDIRALNVHRDHIGVWSQEPVLTGTTISNNIKYGRDDVTDEEMERAREANAYD	60	
Qy	61	FIMEFPNKFTLVGKGAQMSGGQKQRIARALVKNPKILILDEATSAIDSEKSAVQA	120	
Db	61	FIMEFPNKFTLVGKGAQMSGGQKQRIARALVKNPKILILDEATSAIDSEKSAVQA	120	
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Db	121	ALEKASGKGTIVVAHRLSTIRSDIIVTLKQMLAEKGAHAEKGLVYSLVMSQDI	180	
Qy	181	KKADEQMSMTYSTERTKNSLPLHSVKSIKNSDFIDKABESTQSKISLPEVSLKILKLN	240	

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Db 241 KPWPFFVLGTLASVLNGTVHPVPSIIIFAKIITMFGNNDKTTLKHDAAEYISMIFVLGVI 300
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Db 301 CFVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTLTILADIAOI 360
Qy 361 QGATGSRIGVLTONATNMGLSVIISFYGWEMTFLILSIAPVAVTGMETAAVTGPAK 420
Db 361 QGATGSRIGVLTONATNMGLSVIISFYGWEMTFLILSIAPVAVTGMETAAVTGPAK 420
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Db 541 AHLFALLEKKPNIDRSQEGKKPDTCEGNLEFREVSFFPCRPDVFILRGLSLSIERGKT 600
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Db 601 VAFVSSGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPOEPVLVNC 660
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Db 721 IARALLQKPKILLDEATSALENDSEKVVQHALDKARTGRTCLVTVTHRLSAIQNADLIIV 780
Qy 781 LHNGKIKEQGTQHELNRNDIYFKLVNAQSVQ 812
Db 781 LHNGKIKEQGTQHELNRNDIYFKLVNAQSVQ 812

RESULT 2
US-09-873-409-4
; Sequence 4, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE REFERENCE: 81394/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1058
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: No. US20020037522A1e
; LOCATION: (66)...(66)
; OTHER INFORMATION: Xaa at position 66 represents any L amino acid
US-09-873-409-4
Query Match 100.0%; Score 4079; DB 9; Length 1058;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 307 FIMSPFNKNTLVGKGAQMSGQKQRIAIARALVRNPKILILDEATSALESDSESASVOA 366
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Db 367 ALEKASKGRTTIVVAHRLSTIRSDLIIVTLKQMLAEKGAHAELMAKRLGLVYSLVMSQDI 426
Qy 181 KKADEQESMTYSTERTKNSLPLHSVKSISKDSFDKAEESTQSKBISLPEVSLKILKLN 240
Db 427 KKADEQESMTYSTERTKNSLPLHSVKSISKDSFDKAEESTQSKBISLPEVSLKILKLN 486
Qy 241 KPWPFFVLGTLASVLNGTVHPVPSIIIFAKIITMFGNNDKTTLKHDAAEYISMIFVLGVI 300
Db 487 KPWPFFVLGTLASVLNGTVHPVPSIIIFAKIITMFGNNDKTTLKHDAAEYISMIFVLGVI 546
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Db 547 CFVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTLTILADIAOI 606
Qy 361 QGATGSRIGVLTONATNMGLSVIISFYGWEMTFLILSIAPVAVTGMETAAVTGPAK 420
Db 607 QGATGSRIGVLTONATNMGLSVIISFYGWEMTFLILSIAPVAVTGMETAAVTGPAK 666
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Db 667 DKQELKHAGKIATEALENIRTIIVSLTREKAFQMYEEMLOTQHRNTSKKAIIGSCYAFS 726
Qy 481 HAPIFYAAGFRGAYLIQAGRMTPGEMPIVFTALAYGAMAIGKTLVLAPEYSKAKSGA 540
Db 727 HAPIFYAAGFRGAYLIQAGRMTPGEMPIVFTALAYGAMAIGKTLVLAPEYSKAKSGA 786
Qy 541 AHLFALLEKKPNIDRSQEGKKPDTCEGNLEFREVSFFPCRPDVFILRGLSLSIERGKT 600
Db 787 AHLFALLEKKPNIDRSQEGKKPDTCEGNLEFREVSFFPCRPDVFILRGLSLSIERGKT 846
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Qy 721 IARALLQKPKILLDEATSALENDSEKVVQHALDKARTGRTCLVTVTHRLSAIQNADLIIV 780
Db 967 IARALLQKPKILLDEATSALENDSEKVVQHALDKARTGRTCLVTVTHRLSAIQNADLIIV 1026
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; Sequence 6, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE REFERENCE: 81394/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 1195
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-873-409-6

Query Match 100.0%; Score 4079; DB 9; Length 1195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 KPWPFPVLGTASVLNGTVHPVFSIFAKIITMFGNNDKTTLKHDAAEYYSIMFVLGVI 300
DB 624 KPWPFPVLGTASVLNGTVHPVFSIFAKIITMFGNNDKTTLKHDAAEYYSIMFVLGVI 683

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DB 684 CPVSYFMQGLFYGRAGEILTMRLHAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 743

QY 361 QGATGSRIGVLTQNTATNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGANK 420
DB 744 QGATGSRIGVLTQNTATNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGANK 803

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DB 804 DKQELKHAGKIATEALENIRTVSLTREKAFQEMYLEMLOTHRNTSKKAOIIGSCYAFS 863

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DB 864 HAFIYFAYAGFRFGAYLTOAGRMTPGEMFIVFTTAIYAGAMAIGKTLVLAPYSKAKSGA 923

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DB 924 AHLFALLEKKPNIDSRQSKGKPDTCENLRFREVSFFPCRPDPVFLRGLSLSTERGKT 983

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DB 984 VAFVSGGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 1043

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DB 1044 SIAENIAYGNSRVVPLDEIKEAANAANIHSPFIEGLPEKYNTOVGLKGAQLSGGQKORLA 1103

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DB 1104 IARALLQKPKILLDEATSDALNDSKVVQVHALDKARTGTCCLVVTTHRLSAIONADLIYV 1163

QY 781 LHNGKIKQEGTHQELLNRDIIYFKLVNAQSVQ 812
DB 1164 LHNGKIKQEGTHQELLNRDIIYFKLVNAQSVQ 1195

RESULT 4

US-09-873-409-5
; Sequence 5, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611

CURRENT APPLICATION NUMBER: US/09/873,409
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 1222
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: No. US20020037522A1e
LOCATION: (230)..(230)
OTHER INFORMATION: Xaa at position 230 represents any L amino acid
US-09-873-409-5

Query Match 100.0%; Score 4079; DB 9; Length 1222;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 411 MYDENIRALNVHRHYRDHIGVVSQEPVLFQTTISNNIKYGRDDVTDDEMERAAAREANAYD 470

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DB 471 FINEFPNKFNTLVGEGKQMSGGQKQRIARALVRNPKILILDEATSALDSSEKSAVOA 530

QY 121 ALEKASKGRTTIVVAHRLSTIRSGADIVTLKQGMLEAKGAHAELMAKRGLYYSLVMSQDI 180
DB 531 ALEKASKGRTTIVVAHRLSTIRSGADIVTLKQGMLEAKGAHAELMAKRGLYYSLVMSQDI 590

QY 181 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 240
DB 591 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 650

QY 241 KPWPFPVLGTASVLNGTVHPVFSIFAKIITMFGNNDKTTLKHDAAEYYSIMFVLGVI 300
DB 651 KPWPFPVLGTASVLNGTVHPVFSIFAKIITMFGNNDKTTLKHDAAEYYSIMFVLGVI 710

QY 301 CPVSYFMQGLFYGRAGEILTMRLHAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 360
DB 711 CPVSYFMQGLFYGRAGEILTMRLHAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 770

QY 361 QGATGSRIGVLTQNTATNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGANK 420
DB 771 QGATGSRIGVLTQNTATNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGANK 830

QY 421 DKQELKHAGKIATEALENIRTVSLTREKAFQEMYLEMLOTHRNTSKKAOIIGSCYAFS 480
DB 831 DKQELKHAGKIATEALENIRTVSLTREKAFQEMYLEMLOTHRNTSKKAOIIGSCYAFS 890

QY 481 HAFIYFAYAGFRFGAYLTOAGRMTPGEMFIVFTTAIYAGAMAIGKTLVLAPYSKAKSGA 540
DB 891 HAFIYFAYAGFRFGAYLTOAGRMTPGEMFIVFTTAIYAGAMAIGKTLVLAPYSKAKSGA 950

QY 541 AHLFALLEKKPNIDSRQSKGKPDTCENLRFREVSFFPCRPDPVFLRGLSLSTERGKT 600
DB 951 AHLFALLEKKPNIDSRQSKGKPDTCENLRFREVSFFPCRPDPVFLRGLSLSTERGKT 1010

QY 601 VAFVSGGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 660
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QY 721 IARALLQKPKILLDEATSDALNDSKVVQVHALDKARTGTCCLVVTTHRLSAIONADLIYV 780
DB 1131 IARALLQKPKILLDEATSDALNDSKVVQVHALDKARTGTCCLVVTTHRLSAIONADLIYV 1190

QY 781 LHNGKIKQEGTHQELLNRDIIYFKLVNAQSVQ 812
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RESULT 5

US-10-415-378-14
; Sequence 14, Application US/10415378
; Publication No. US20040014945A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, V. Tom
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.;
; APPLICANT: HAFALIA, April J.A.; ELIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: GANDHI, Ameena R.; DING, Li;
; APPLICANT: SANJAWALA, Madhundan M.; RAMKUMAR, Javalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIEZEN, Kimberly J.;
; APPLICANT: LAL, Frecci G.; AZIMZAI, Fajda;
; APPLICANT: KHAN, Farrar A.; THANGAVELOU, Kavitha;
; APPLICANT: THORNTON, Michael B.; LU, Dyrung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0276 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040014945A1 7472030CD1
US-10-415-378-14

Query Match 96.1%; Score 3919; DB 15; Length 1232;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 785; Conservative 1; Mismatches 0; Indels 26; Gaps 1;

QY 1 MVDENDIRALNVRYRHDIGVVSQEPVLFGTISNNIKYGRDDVTDBEMERAREANAYD 60
DB 447 MVDENDIRALNVRYRHDIGVVSQEPVLFGTISNNIKYGRDDVTDBEMERAREANAYD 506
QY 61 FIMEPPKNTLVGKGAQMSGGQKQRIARALVRNPXKILILDEATSALDSSEKSAVQA 120
DB 507 FIMEPPKNTLVGKGAQMSGGQKQRIARALVRNPXKILILDEATSALDSSEKSAVQA 566
QY 121 ALEKASKRTTIVVAHRLSTRSADLIIVTLKQGMALAEKGAHAEKMAKRGLYSLVMSQDI 180
DB 567 ALEKASKRTTIVVAHRLSTRSADLIIVTLKQGMALAEKGAHAEKMAKRGLYSLVMSQDI 626
QY 181 KCADEQMSMTYSTERTKNSPLHSVKSISKSDPFIDKABESTOSKEISLPEVSLKILKLN 240
DB 627 KCADEQMSMTYSTERTKNSPLHSVKSISKSDPFIDKABESTOSKEISLPEVSLKILKLN 686
QY 241 KPEWPFVVLGTLASVLNGTVHPVFSIIIPAKIITMFGNNDKTTLKHDAEIYSMIFVLGVI 300

DB 687 KPEWPFVVLGTLASVLNGTVHPVFSIIIPAKIITMFGNNDKTTLKHDAEIYSMIFVLGVI 746
QY 301 CFVSYFMQGLFYGRAGEILTWELRHAFKAMLYQDIAMFDEKENSTGGTTLTILADIAOI 360
DB 747 CFVSYFM-----QDIAMFDEKENSTGGTTLTILADIAOI 780
QY 361 QGATSGRIGVLTONATNMGLSVIIISFIYGWEMTFLISLAPVLAVTGMETETAAMTGFAK 420
DB 781 QGATSGRIGVLTONATNMGLSVIIISFIYGWEMTFLISLAPVLAVTGMETETAAMTGFAK 840
QY 421 DKQELKHAGKIATEALENIRTIIVSLTREKAPQMEEMLOTOHRTSKKAOIIGSCYAFS 480
DB 841 DKQELKHAGKIATEALENIRTIIVSLTREKAPQMEEMLOTOHRTSKKAOIIGSCYAFS 900
QY 481 HAFIYFAYAAAGFRFGAYLIQAGRWTPGEGFIVFTAIAYGAMAIGETLVLAPEYSKAKSGA 540
DB 901 HAFIYFAYAAAGFRFGAYLIQAGRWTPGEGFIVFTAIAYGAMAIGETLVLAPEYSKAKSGA 960
QY 541 AHLFALLEKKPNIDSRSQGKPDCEGNLEPREVSFFPCRPDPVFIILRGLSLSTERGKT 600
DB 961 AHLFALLEKKPNIDSRSQGKPDCEGNLEPREVSFFPCRPDPVFIILRGLSLSTERGKT 1020
QY 601 VAFVSGSGGKSTSVQLLQRLYDPVQGVLPFGVDKELNVQWLSQIAIVPQEPVLENC 660
DB 1021 VAFVSGSGGKSTSVQLLQRLYDPVQGVLPFGVDKELNVQWLSQIAIVPQEPVLENC 1080
QY 661 STAENIAYGDNRSRVVPLDBIKEAANAANTHSFIEGLPEKINTQVGLKGHQLSGGQKORLA 720
DB 1081 STAENIAYGDNRSRVVPLDBIKEAANAANTHSFIEGLPEKINTQVGLKGHQLSGGQKORLA 1140
QY 721 IARALLQKPKILLDEATSALDNSEKVVQHALDKARTGRTCLVWTHRLSAIQNADLIIV 780
DB 1141 IARALLQKPKILLDEATSALDNSEKVVQHALDKARTGRTCLVWTHRLSAIQNADLIIV 1200
QY 781 LHNGKIKEQGTTHQELLNRNDIYFKLVNAQSVQ 812
DB 1201 LHNGKIKEQGTTHQELLNRNDIYFKLVNAQSVQ 1232

RESULT 6

US-09-873-409-1
; Sequence 1, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-1

Query Match 81.5%; Score 3323; DB 9; Length 659;
Best Local Similarity 100.0%; Pred. No. 1,2e-290; Indels 0; Gaps 0;
Matches 659; Conservative 0; Mismatches 0;

QY 154 MIAEKGAHAEKMAKRGLYSLVMSQDIKKADEQMSMTYSTERTKNSPLHSVKSISKSDF 213
DB 1 MIAEKGAHAEKMAKRGLYSLVMSQDIKKADEQMSMTYSTERTKNSPLHSVKSISKSDF 60
QY 214 IDKABESTOSKEISLPEVSLKILKLNKPEWPFVVLGTLASVLNGTVHPVFSIIIPAKIIT 273
DB 61 IDKABESTOSKEISLPEVSLKILKLNKPEWPFVVLGTLASVLNGTVHPVFSIIIPAKIIT 120
QY 274 MFGNNDKTTLKHDAEIYSMIFVLGVIKPEWPFVQGLFYGRAGEILTWELRHAFKAMLY 333

Db 121 MFGNDKTTLKHDAEYISMIFVLGVICFVSFVMOGLFYGRAGEIILTMRLRLHAFKAMLY 180
Qy 334 QDIAWDEKENSNGGLTTLIAIDIAIQOGATSGRIGVLTONATNMGSLVSIISFIYGEWT 393
Db 181 QDIAWDEKENSNGGLTTLIAIDIAIQOGATSGRIGVLTONATNMGSLVSIISFIYGEWT 240
Qy 394 FLILSIAPVLAVTGMETAMTGFANKDKOELKHAGKIAATEALENIRTIIVSLTREKAFBQ 453
Db 241 FLILSIAPVLAVTGMETAMTGFANKDKOELKHAGKIAATEALENIRTIIVSLTREKAFBQ 300
Qy 454 MYEEMLOTOHNTSKQAIIIGSCVAFSHAFIYFAYAGPRFGAYLQAGRWTPGEMFIYF 513
Db 301 MYEEMLOTOHNTSKQAIIIGSCVAFSHAFIYFAYAGPRFGAYLQAGRWTPGEMFIYF 360
Qy 514 TAIYAGAMAIGKTLVLAPESKAKSAGAAHFLALLEKXPNIDSSQBGKXPDCEGNLEPR 573
Db 361 TAIYAGAMAIGKTLVLAPESKAKSAGAAHFLALLEKXPNIDSSQBGKXPDCEGNLEPR 420
Qy 574 EVSFFPYCRPDVILRGLSLISIRGKTVAFVGSGGCKSTSVOLLQRLYDPVQGVLFQD 633
Db 421 EVSFFPYCRPDVILRGLSLISIRGKTVAFVGSGGCKSTSVOLLQRLYDPVQGVLFQD 480
Qy 634 VDAKELNVQLRSQIAIVPOEPVLFNCISIAENIAYGDNRSRVVPLDEIKEAANAANIESPI 693
Db 481 VDAKELNVQLRSQIAIVPOEPVLFNCISIAENIAYGDNRSRVVPLDEIKEAANAANIESPI 540
Qy 694 EGLPEKNTQVGLKGAQLSGGQKQRIAIARALLQKPKILLDEATGALDNDSEKVVQHAL 753
Db 541 EGLPEKNTQVGLKGAQLSGGQKQRIAIARALLQKPKILLDEATGALDNDSEKVVQHAL 600
Qy 754 DKARTGRTCLVWTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQSVQ 812
Db 601 DKARTGRTCLVWTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQSVQ 659

RESULT 7
US-10-092-900A-304
; Sequence 304, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C

; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 304
; LENGTH: 1354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-304

Query Match 77.7%; Score 3168.5; DB 12; Length 1354;
Best Local Similarity 76.8%; Pred. No. 3.6e-276;
Matches 677; Conservative 30; Mismatches 62; Indels 113; Gaps 14;

Qy 2 VDENDIRALNVHRDHIGVWSQEPVLFGTTTISNIIKVGRRD--VTDEKESAAAREANAY 59
Db 455 VDGVDKELNVQLRSQIAIVPOEPVLFNCISIAENIAYGDNRSRVVPLDEIKEAANAANIH 514
Qy 60 DEIMFPNKFNTLVGSKGAGMSGGQKQRIAIARALRNPKIILDEATSEK-SAV 118
Db 515 SFIEGLPEKNTQVGLKGAQLSGGQKQRIAIARALLQKPKILLDEATSEK-SALONDSQV 574
Qy 119 QAALEK----- 124
Db 575 QHALDKARTGRTCLVWTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQ 634
Qy 125 -ASKGRTTIWAHRLSTIRSDLIIVTLKDGMLAEKGAHAELMAKXGLYYSLVMSQDIKKA 183
Db 635 SASKGRTTIWAHRLSTIRSDLIIVTLKDGMLAEKGAHAELMAKXGLYYSLVMSQ----- 689
Qy 184 DEQMESMTYSTRKTNLSPLHSVKSISKDFIDKABESTQSKEISLPEVSLKILKLNKPE 243
Db 690 -----VLMGTLSDCGN-----SLPEVSLKILKLNKPE 718
Qy 244 NPPVVLGTLASVLNGTVHVPFSIIIAKIIIT-MFGNNDKTTLKHDAEIIYSMIFVLGV--- 299
Db 719 NPPVVLGTLASVLNGTVHVPFSIIIAKIIITVMPGNND---LFFFLKIFLYSLFLPKOG 775
Qy 300 --ICPVSVFMOGLFYGRAGEIILTMRLRLHAFKAMLYQDIAWDEKENSTGGLTTLIAIDI 357
Db 776 FSVDFCLPFAQGLFYGRAGEIILTMRLRLHAFKAMLYQDIAWDEKENSTGGLTTLIAIDI 835
Qy 358 AOIQGATGSRIGVLTONATNMGSLVSIISFIYGEWTFLILSIAPVLAVTGMETAMTGF 417
Db 836 AOIQGATGSRIGVLTONATNMGSLVSIISFIYGEWTFLILSIAPVLAVTGMETAMTGF 895
Qy 418 ANKDKOELKHAG--KIATEALENIRTIIVSLTREKAPQMEYEMLOTOH-RNTSKQAIIIG 474
Db 896 ANKDKOELKHAGKVIATEALENIRTIIVSLTREKAPQMEYEMLOTOHRRNTSKQAIIIG 955
Qy 475 SCYAFSHAFIYFAYAGPRFGAYLQAGRWTPGEMF-IVFTAIYAGAMAIGKTLVLAPSY 533
Db 956 SCYAFSHAFIYFAYAGPRFGAYLQAGRWTPGEMF-IVFTAIYAGAMAIGKTLVLAPSY 1015

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QY 534 SKAKGAHLFALLEKXPNIDSRQEGKP---DTCENLRETFREVFYPCREDVPIRG 590
DB 1016 SKAKGAHLFALLEKXPNIDSRQEGKPLSQDTCEGNLETFREVFYPCREDVPIRG 1075
QY 591 LSLISIERGKTVAFVSSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAI 650
DB 1076 LSLISIERGKTVAFVSSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAI 1135
QY 651 VPOEPVLFNCISAEINAYGNSRVVPLDEIKEAANAANHSFIEGPEKYNTOVGLKGAQ 710
DB 1136 VPOEPVLFNCISAEINAYGNSRVVPLDEIKEAANAANHSFIEGLP-KYNTQVGLKGAQ 1194
QY 711 LSGGQKORLAIALALOKPKILLDEATSDNDSEK--VVQHALDKARTGRTCLVWVTHR 768
DB 1195 LSGGQKORLAIALALOKPKILLDEATSDNDSEKVVQVQHALDKARTGRTCLVWVTHR 1254
QY 769 LSAIQNADLIIVLHNGKIKQGTQHELLRNDRDIYFKLVNAQS 810
DB 1255 LSAIQNADLIIVLHNGKIKQGTQHELLRNDRDIYFKLVNAQS 1296

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RESULT 8

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US-09-817-762-5
; Sequence 5, Application US/09817762
; Publication No. US20020068344A1
; GENERAL INFORMATION:
; APPLICANT: Spalding, Edgar P.
; APPLICANT: Non, Bosi
; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P21439
; DATABASE ENTRY DATE: 1998-07-15
US-09-817-762-5

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Query Match 60.4%; Score 2465.5; DB 12; Length 1066;
Best Local Similarity 58.3%; Pred. No. 7.3e-213;
Matches 478; Conservative 149; Mismatches 182; Indels 11; Gaps 3;

QY 2 VDENDIRALNVRYDRHIGVVSQEPVLPFGTTISNNIKYGRDVTDEEMERAAREANAYDF 61
DB 242 IDGQDIRNFNVNLYREIIGVVSQEPVLPFGTTISNNIKYGRDVTDEEMERAAREANAYDF 301
QY 62 IMEPNFKNTLVGKGAQMSGGQKORLAIALALVNPKNILDEATSDSEKSAVQAA 121
DB 302 IMKLPQKFDTLVGRGAQMSGGQKORLAIALALVNPKNILDEATSDSEKSAVQAA 361
QY 122 LKAKGRITTVIARLSTIRADLIIVLTKGMAEKGAHAELMAKRGVYSLV----- 175
DB 362 LKAKGRITTVIARLSTIRADLIIVLTKGMAEKGAHAELMAKRGVYSLV----- 421
QY 176 ----MSQDIKABQEMESMTYSTERKTNLSPLHSVKSIIK-SDFIDKA-BESTQSKEISLPE 230
DB 422 SQTQSEFEFLNDEKATRNAPNGWKSRLFRHSTQKNLNSQMSQKSLDVTGDLGANVPP 481
QY 231 VSLIKTLKLNKBPWPVVLGTLASVLNGTVHPVPSIIIPAKIITFMGNNDKTKTLKHDAIY 290
DB 482 VSLFKVLKLNKBPWPVVLGTLASVLNGTVHPVPSIIIPAKIITFMGNNDKTKTLKHDAIY 541

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QY 291 SMIFVLGVICFVSFMOGLFYGRAGEILTWELRHAEKAMLYODIAMPDEKENSTGGIT 350
DB 542 SMIFVLGVICFVSFMOGLFYGRAGEILTWELRHAEKAMLYODIAMPDEKENSTGGIT 601
QY 351 TILALIDIAIQCATGSRICVLQTNATNMGLSVIIISFIYGWMTFLILSIAPVLAVTGMIE 410
DB 602 TILALIDIAIQCATGSRICVLQTNATNMGLSVIIISFIYGWMTFLILSIAPVLAVTGMIE 661
QY 411 TAAMTGPANKQOELKHAGKINATEALENRTIVSLTREKAFQMYEEMLQTOHRNTSKA 470
DB 662 MGLLAGNAKRDKKLEAGAKIATEAENIRTVSUTQERKFSMIVKLYGPRNSVQKA 721
QY 471 QIIGSCYAFSHAFIYFAVAAGFRFGAYITQAGMTPEGMPIVFTAIYAGAMAIGKTLVA 530
DB 722 HIYGITPISQAFMYFSYAGCFRFGAYLIVNGHMERDVLVFSALVFGAVALGHASSPA 781
QY 531 PYSYAKSAAHLFALLEKXPNIDSRQEGKPDTCENLRETFREVFYPCREDVPIRG 590
DB 782 PYSYAKSAAHLFALLEKXPNIDSRQEGKPDTCENLRETFREVFYPCREDVPIRG 841
QY 591 LSLISIERGKTVAFVSSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAI 650
DB 842 LSLISIERGKTVAFVSSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAI 901
QY 651 VPOEPVLFNCISAEINAYGNSRVVPLDEIKEAANAANHSFIEGPEKYNTOVGLKGAQ 710
DB 902 VPOEPVLFNCISAEINAYGNSRVVPLDEIKEAANAANHSFIEGPEKYNTOVGLKGAQ 961
QY 711 LSGGQKORLAIALALOKPKILLDEATSDNDSEKVVQVQHALDKARTGRTCLVWVTHR 770
DB 962 LSGGQKORLAIALALOKPKILLDEATSDNDSEKVVQVQHALDKARTGRTCLVWVTHR 1021
QY 771 AIQNADLIIVLHNGKIKQGTQHELLRNDRDIYFKLVNAQS 810
DB 1022 AIQNADLIIVLHNGKIKQGTQHELLRNDRDIYFKLVNAQS 1061

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RESULT 9

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US-10-363-112-49
; Sequence 49, Application US/10363112
; Publication No. US20040091964A1
; GENERAL INFORMATION:
; APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY
; APPLICANT: BOARD, PHILLIP
; APPLICANT: HARRIS, MATTHEW
; TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
; FILE REFERENCE: 007643-0302189
; CURRENT APPLICATION NUMBER: US/10/363,112
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/AU01/01093
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,663
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 1275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-112-49

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Query Match 60.4%; Score 2465.5; DB 16; Length 1275;
Best Local Similarity 58.3%; Pred. No. 9.9e-213;
Matches 478; Conservative 149; Mismatches 182; Indels 11; Gaps 3;

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QY 2 VDENDIRALNVRYDRHIGVVSQEPVLPFGTTISNNIKYGRDVTDEEMERAAREANAYDF 61
DB 455 IDGQDIRNFNVNLYREIIGVVSQEPVLPFGTTISNNIKYGRDVTDEEMERAAREANAYDF 514
QY 62 IMEPNFKNTLVGKGAQMSGGQKORLAIALALVNPKNILDEATSDSEKSAVQAA 121
DB 515 IMKLPQKFDTLVGRGAQMSGGQKORLAIALALVNPKNILDEATSDSEKSAVQAA 574

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; SEQ ID NO 8
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-101-433A-8

Query Match      59.9%; Score 2442; DB 14; Length 1281;
Best Local Similarity 56.8%; Pred. No. 1.3e-210;
Matches 469; Conservative 160; Mismatches 178; Indels 18; Gaps 4;

QY 2 VDENDIRALNVRYRHHGIVVQSPVLFGTTISNNIKYGRDDVTDDEMERAAERANAYDF 61
DB 455 IDGQDIRTINVRLREITGVVQSPVLFGTTIAENIRYGRNVTDDEIEKAVKANAYDF 514
QY 62 IMEPNKNFTLVGKGAOMSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 121
DB 515 IMKLPNKFDTLVGERGAQLSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 574
QY 122 LEKAKGRRTTIVVAHRLSTIRADLIIVTLKGMKAEKGAHAEKAGLYIYSLVMSQDIK 181
DB 575 LDKARKGRRTTIVIAHRLSTVRNADVIAGFDGVIVEXGNHDELMKEKGIYFKLVMTQ-TR 633
QY 182 KADQESMTYSTERTKNSLPLHSVKSIKSDFI-----DKAESSTOSKEI 226
DB 634 GNEIELENATGESKESDALEM-SPKDSGSLIKRSTRSIIHAPQGDRLGTEDLNE 692
QY 227 SLPEVSLKILKLNKPEWPFVVLGTSLASVLTNGTVHPVFSIIFAKIITMF-GNNDKTTLKH 285
DB 693 NVPPVSFWRLKLNSTWEPYFVVGIFCAIINGGLQPAFSIIFSRIGIFTRDEDPETKQ 752
QY 286 DAEIVSMIFVLGICVSVFMQGLFYGRAGEILTMRLHLAKMAYODIAWFDKENS 345
DB 753 NSNMFSLVLGIGIISITIFLQGTFFKAGEILTKRLIWMFRSLRQDVSWFDDPKNT 812
QY 346 TGGTTLTILADIAIQGATSGRIGVLTONATNMGSLVSIISFYGMWTFILISIAPLAV 405
DB 813 TGAUTRLANDAQAQVKAIGSRLAVITONIANLGTGIIISLIYQWLTLLLAIVPIAI 872
QY 406 TGMETAAATGANKDKQELKAGKIATEALENIITVSLTREKAPQWYEMLOTHRN 465
DB 873 AGVVEKMLSGQALKDKKELEGAGKIATEALENFRITVVSUTREOKPEYMTAQSLOVPYRN 932
QY 466 TSKAQIIGSCYAFSHAFIYFAYAGFRFGAYLIQAGRMTPEGMTFIVFTAIAYGAMAIGK 525
DB 933 SLRKAHIFGVFSITQAMWYFSYAGCFRFGAYLVANEFMNFQDVLVFSALVFGAMAVGQ 992
QY 526 TLVLAPYSKAKSGAAHLFALLEKPNIDRSQEGKPDTCGNLEFRYSFYPCEPDV 585
DB 993 VSSPAPDYAKAVGAAHVIMIIEKSPIDISYSPHGLKPNTEGNTFENVEVNYTPRDI 1052
QY 586 FILRGLSLIERGKTAVFVSGSGCGKSTSVOLLQRLYDPVQGVLPDGVDAKELNVQWLR 645
DB 1053 PVLQGLSLEVKGQTLALVSGSGCGKSTVVQLLERFYDPLAGSVLIDGKEIKHLNVQWLR 1112
QY 646 SQIAIVQPEPVLFNCSIAENIAYGNSRWVPLDEIKEAANAANIHSFIEGLPEKYNTOVG 705
DB 1113 AHLGIVSQEPILFDCSIAENIAYGNSRWVSHBEIMOAKAANIHHFIETLPEKYNTRVG 1172
QY 706 LKGAQLSGGQKORIAIARALVRNPKILILDEATSALDNDSEKVVQHALDKARTGRTCLV 765
DB 1173 DKGTLQSGGQKORIAIARALVRNPKILILDEATSALDSEKVVQHALDKAREGRTCIVI 1232
QY 766 THRLSAIQNADLIIVLHNGKIKEQTHQELLNRDIYFKLVNAQS 810
DB 1233 AHRLLSTIQNADLIIVFQNGKVKERHGTQOILLAQKGIYFSKVSQA 1277

RESULT 12
US-10-101-433A-9
; Sequence 9, Application US/10101433A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara
```

Db 1233 AHRSTLSTQNADLIWVFGKVKRKHGTHQQLAOKGIYFSMVSVQA 1277

RESULT 13

US-09-769-097-2

Sequence 2, Application US/09769097

Patent No. US20020055128A1

GENERAL INFORMATION:

APPLICANT: Kimberly Anne Brun

APPLICANT: Richard James Chenery

APPLICANT: Harma Ellens

APPLICANT: John Anthony Feild

APPLICANT: Lin Yue

TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES

FILE REFERENCE: GP-50009-C2

CURRENT APPLICATION NUMBER: US/09/769,097

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/208,809

PRIOR FILING DATE: 1998-12-09

PRIOR APPLICATION NUMBER: 09/156,800

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: US99/20770

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1272

TYPE: PRT

ORGANISM: RATTUS RATTUS

US-09-769-097-2

Query Match 59.8%; Score 2441; DB 9; Length 1272;

Best Local Similarity 57.1%; Pred. No. 1.6e-210;

Matches 470; Conservative 164; Mismatches 175; Indels 14; Gaps 5;

Qy 2 VDENDIRALNVRHYRDHIGVVSQEPVLTGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 61

Db 445 IDGQDRTINVRYLREIIGVVSQEPVLTGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 504

Qy 62 IMEFNPKNTLVGKGAQSGGKQRIARALVRNPKILILDEATSDLSSEKSAVQAA 121

Db 505 IMKLPHKEDTLVGERGAQLSGGKQRIARALVRNPKILILDEATSDLSSEKSAVQAA 564

Qy 122 LEKASGRTTIVVHRLSTIRSDIIVTLKDGMLAEKAHAELMAKRGILYSLVMSQ--- 178

Db 565 LDKAREGRTTIVIAHRLSTVRNADYVAGDGGVIVGQGHDELAKREKGIYFKLVMTQTAG 624

Qy 179 -DIKKADEQMBES-----MTYSTERTKNSL--PLHSVKSISKDFIDKABEST-OSKEISL 228

Db 625 NEIELGNACESKDGIDNVDMSSKDSGLIRRRSTRKIRGPHDQDGLSTKEALDDVD 684

Qy 229 PEVSLKILKLNKPEWPFVVLGTSLASVLTGTVHPVFSIIFAKIIITWFGNNDKTTL-KHDA 287

Db 685 PPASFWRILKLNSTWPFVVGVCFAINGGLQPAFSAIIFSKVVGFTKNDTPETQONS 744

Db 1233 AHRSTLSTQNADLIWVFGKVKRKHGTHQQLAOKGIYFSMVSVQA 1277

RESULT 13

US-09-769-097-2

Sequence 2, Application US/09769097

Patent No. US20020055128A1

GENERAL INFORMATION:

APPLICANT: Kimberly Anne Brun

APPLICANT: Richard James Chenery

APPLICANT: Harma Ellens

APPLICANT: John Anthony Feild

APPLICANT: Lin Yue

TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES

FILE REFERENCE: GP-50009-C2

CURRENT APPLICATION NUMBER: US/09/769,097

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/208,809

PRIOR FILING DATE: 1998-12-09

PRIOR APPLICATION NUMBER: 09/156,800

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: US99/20770

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1272

TYPE: PRT

ORGANISM: RATTUS RATTUS

US-09-769-097-2

Query Match 59.8%; Score 2441; DB 9; Length 1272;

Best Local Similarity 57.1%; Pred. No. 1.6e-210;

Matches 470; Conservative 164; Mismatches 175; Indels 14; Gaps 5;

Qy 2 VDENDIRALNVRHYRDHIGVVSQEPVLTGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 61

Db 445 IDGQDRTINVRYLREIIGVVSQEPVLTGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 504

Qy 62 IMEFNPKNTLVGKGAQSGGKQRIARALVRNPKILILDEATSDLSSEKSAVQAA 121

Db 505 IMKLPHKEDTLVGERGAQLSGGKQRIARALVRNPKILILDEATSDLSSEKSAVQAA 564

Qy 122 LEKASGRTTIVVHRLSTIRSDIIVTLKDGMLAEKAHAELMAKRGILYSLVMSQ--- 178

Db 565 LDKAREGRTTIVIAHRLSTVRNADYVAGDGGVIVGQGHDELAKREKGIYFKLVMTQTAG 624

Qy 179 -DIKKADEQMBES-----MTYSTERTKNSL--PLHSVKSISKDFIDKABEST-OSKEISL 228

Db 625 NEIELGNACESKDGIDNVDMSSKDSGLIRRRSTRKIRGPHDQDGLSTKEALDDVD 684

Qy 229 PEVSLKILKLNKPEWPFVVLGTSLASVLTGTVHPVFSIIFAKIIITWFGNNDKTTL-KHDA 287

Db 685 PPASFWRILKLNSTWPFVVGVCFAINGGLQPAFSAIIFSKVVGFTKNDTPETQONS 744

Qy 288 EIVSMIFVILGVCFSYFMOGLFYGRAGSILTMRLHLAFKAMLYQDIAMFDEKENSTG 347

Db 745 NLFSLFLIILGISFTTFFLQGTFFGKAGSILTKRLRYMFKSMRLQDISWFDPKNTTG 804

Qy 348 GLTILAILDAIQCATGSGIGVLITQWATNGLSVLSIISPIYGHWTFFLISLAPVLAVTG 407

Db 805 ALTRLANDAAQKAGTSGSLAVITQNIAMGLGIIISLIYQGLTLLAILVPIIATAG 864

Qy 408 MIETAMTGFANDKQELKHAGKIAETALEINIRITVSLTRKAFEQWYEMLOTOHRTS 467

Db 865 VVEMQMSGLAKDKKLEGGSKIAETAIENFTVVSILTEEQKEFTWYAGSLQIPIYNAL 924

Qy 468 KKAQIGSCVAFSHAFYFAYAGFRPGATLIQAGRTWPEGMFTVITAYAGMAIGKTL 527

Db 925 KKAHVFGITTSFTQAMMYFSAACFRFDAYLVARELMTFENVLLVFSALVFGAMVQVS 984

Qy 528 VLAPEYSKAKSAAHLLFALLEKKPNIDRSQEGKKPDTCEGNLEPREVSFFFCRDPVFI 587

QY 288 EIIYSMIFVILGVICFVSFMOGLFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 347
 DB 745 NLFSLFLILGIIISFIFLQGFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 804
 QY 348 GLTTLAIDIAIQOATGSRIGVLTQATNMGSLVSIISFYIYVEMTFLIISIAFVAVTG 407
 DB 805 ALTLRLANDAAQVKGATRLAVITQNTANLGTGIIISLIYVEMTFLIISIAFVAVTG 864
 QY 408 MIETAMTGFANKQKQELKHAGKIATEALENIRIVSLTREKAFQEMVEMLOTHQHNST 467
 DB 865 VYEMKMLSGQALDKKXLEGSGKIATEALENIRIVSLTREKAFQEMVEMLOTHQHNST 924
 QY 468 KKAQIIIGSCYAFSHAFIYFAAAGFRFGAYLIQAGRTPEGMFTVFTAIAYGAMAIGKTL 527
 DB 925 KKAHVGITFTSQAMWYFSAACFRPDALVARELMTFENVLVFSALVFGANAVQVS 984
 QY 528 VLAPEYSKAKSGAHLFALLKXKNIIDRSQEGKKPDTCEGNLEFREVSPYPCRPDVFI 587
 DB 985 SFAPQYAKAKVSASHIIRIEIKPIIDSYSTEGKPNMLEGVFNKGVNMFNPTRPNIPV 1044
 QY 588 LRGLSLSTERGKTIVAFVSGSGCKSTSVQLLQRLYDVPQGVLFQDGVDAKELNVQWLR 647
 DB 1045 LQGLSLEVKKQTLALVSGSGCKSTSVQLLQRLYDVPQGVLFQDGVDAKELNVQWLR 1104
 QY 648 IAVPQEPVLPNCSTIAENIAYGDNRSRVVPLDEIKKAAANAHIHSFIEGLPEKYNQVGLK 707
 DB 1105 LGIVSQEPILFDCSLAENIAYGDNRSRVVSHKEIVKAAKEANIHOPIIDSLPKYNTRVGDK 1164
 QY 708 GAOLSGGOKORLAIARALLQKPKILLDEATSDNDSEKVVQHALDKARTGRTCLVYTH 767
 DB 1165 GQLSGGOKQRIARALVRPHILLDEATSDNDSEKVVQHALDKARTGRTCLVYTH 1224
 QY 768 RLSTATIONADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 810
 DB 1225 RLSTATIONADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 1267

RESULT 15
 US-10-101-433A-3
 ; Sequence 3, Application US/10101433A
 ; Publication No. US20030119726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanscom, Sara
 ; APPLICANT: Crespi, Charles
 ; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
 ; FILE REFERENCE: G00307/70019
 ; CURRENT APPLICATION NUMBER: US/10101433A
 ; CURRENT FILING DATE: 2002-03-19
 ; PRIOR APPLICATION NUMBER: US 60/277,095
 ; PRIOR FILING DATE: 2001-03-19
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1280
 ; TYPE: PRT
 ; ORGANISM: Macaca fascicularis
 US-10-101-433A-3

Query Match 59.8%; Score 2441; DB 14; Length 1280;
 Best Local Similarity 56.4%; Pred. No. 1.6e-210;
 Matches 465; Conservative 168; Mismatches 174; Indels 18; Gaps 5;

QY 2 VDENDIRALNVHRDHIGVWSQEPVLPFGTITSNKIKYGRDDVDTEEMERARANAYDF 61
 DB 453 VQGDRTINLVFLREIIGVWSQEPVLPFATIAENIRYGRDVTWDEIEKAVKEANAYDF 512
 QY 62 IMEPNKNWTLVGEKGAQNSGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 121
 DB 513 INKLQKFTLVGERGAQLSGGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 572
 QY 122 LEKASKGRTIIVVHRLSTIRADLIIVLQKQMLAEKGAHAEIMAKRGLIYSLVMSQDI- 180
 DB 573 LDKARKGRTIIVVHRLSTIRADLIIVLQKQMLAEKGAHAEIMAKRGLIYSLVMSQDI- 632

QY 181 -----KKADE---QMESMTYSTERKTNLSL-----PLHSVKSIKSDPIDKABESTOSKEI 236
 DB 633 NEIELENAADESKSEIDITLEMSSHDSGLIRKSTRSRVRSQGG--DRKLSTKALDE 690
 QY 227 SLPEVSLKILKLNKPEWPFVVLGTILASVLNGTVHPVFSIIIFAKIITMF-GNNDKTTLKH 285
 DB 691 SIPPVSFWRIMKLNLTWEPYFVGVPCALINGLOPAFAVIFSKIIIGIETFRNDDAETKRQ 750
 QY 286 DAEIYSMIIVILGVICFVSFMOGLFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENST 345
 DB 751 NSLFLSLLFLVLGVISFIFTFQGFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENST 810
 QY 346 TGLTTLAIDIAIQOATGSRIGVLTQATNMGSLVSIISFYIYVEMTFLIISIAFVAVTG 405
 DB 811 TGLTTLRLANDAAQVKGATRLAVITQNTANLGTGIIISLIYVEMTFLIISIAFVAVTG 870
 QY 406 TGMETAMTGFANKQKQELKHAGKIATEALENIRIVSLTREKAFQEMVEMLOTHQHNST 465
 DB 871 AGVEMKMLSGQALDKKXLEGSGKIATEALENIRIVSLTREKAFQEMVEMLOTHQHNST 930
 QY 466 TSKKAOIIIGSCYAFSHAFIYFAAAGFRFGAYLIQAGRTPEGMFTVFTAIAYGAMAIGK 525
 DB 931 SLRKAHIFGITFTSQAMWYFSAACFRPDALVARELMTFENVLVFSALVFGANAVQ 990
 QY 526 TVLAPEYSKAKSGAHLFALLKXKNIIDRSQEGKKPDTCEGNLEFREVSPYPCRPDV 585
 DB 991 VSSFAPDYAKAKVSAASHIIRIEIKPIIDSYSTEGKPNMLEGVFNKGVNMFNPTRPNIPV 1050
 QY 586 FILRGLSLSTERGKTIVAFVSGSGCKSTSVQLLQRLYDVPQGVLFQDGVDAKELNVQWLR 645
 DB 1051 PVLQGLSLEVKKQTLALVSGSGCKSTSVQLLQRLYDVPQGVLFQDGVDAKELNVQWLR 1110
 QY 646 SQIAIYVQEPVLPNCSTIAENIAYGDNRSRVVPLDEIKKAAANAHIHSFIEGLPEKYNQV 705
 DB 1111 AHLGISVQEPILFDCSLAENIAYGDNRSRVVSHKEIVKAAKEANIHOPIIDSLPKYNTRVG 1170
 QY 706 LKGAOLSGGOKORLAIARALLQKPKILLDEATSDNDSEKVVQHALDKARTGRTCLVY 765
 DB 1171 DRGTQLSGGOKQRIARALVRPHILLDEATSDNDSEKVVQHALDKARTGRTCLVY 1230
 QY 766 THRLSAIONADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 810
 DB 1231 ARLSTIONADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 1275

Search completed: June 24, 2004, 15:24:03
 Job time : 53 secs


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Db 751 NSNLSLLFLVLGIVSFTTFLQGFPGKAGEIILTKRLRYMVFMSMLRQDVSNFDDPKNT 810
Qy 346 TGGTTLTILADIAIOGATSGRIGVLTQNTATNMGSLVIIISFYGEMTFLILSIAPVLAV 405
Db 811 TGAITRILANDAAQVKGAIKSLRLAIITQNTANLGTGIIISLVGQTLTLLLAIVPIIAL 870
Qy 406 TGMTETAMTGFANKQBLKHAQKIATEALENIRTVSLTRKAFQMYEEMLOTOHRN 465
Db 871 AGVYEMXLSQALUKDKLEGAGKIATEAIENFRITVVSUTQEQKFPHMYDQSLQVPYRN 930
Qy 466 TSKAQIIGSCYAFSHAFIYFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 525
Db 931 SLRKAHIFGITFTQAMMYFAYAGFRFGAYLVAHSLMSFEDVLLVFSAVFGAMAVGQ 990
Qy 526 TLVLAPYSKAKSAAHLFALLEKKPNIDSRQKGPDTCEGNLBRFVSFFYPCRPDV 585
Db 991 VSSPAPDYAKAKVSAHHIIMIEKTPLDISTYSTGLKPNTEGNTFNEVFNYPTRLDI 1050
Qy 586 FILGSLISIERGKTVAFFVSGSGGKSTVOLLORLYDPVQGVLDGDAKELAVOWLR 645
Db 1051 PVLQGLSLEVKKGQTLALVSGSGGKSTVOLLBRFYDPLAGKVLLOGKEIKQLNVQWLR 1110
Qy 646 SOIAIVPOBPVLPNCSTAEINAYGNSRWVFLDBIKAAANAANTHSFIEGLPEKINTQVG 705
Db 1111 AHLGIVSQEPILFDCSISEINAYGNSRWVSEIIVRAAKEANIHAFIESLPNKYSTRVG 1170
Qy 706 LKGAQLSGGQKQRIALARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 765
Db 1171 DKGTLQSGGQKQRIALARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 1230
Qy 766 THRLSAIQNADLIVVFNQGRVKEHGTQQLLAQKGIYFSMVVQA 810
Db 1231 AHRSTIQNADLIVVFNQGRVKEHGTQQLLAQKGIYFSMVVQA 1275

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RESULT 2

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US-09-672-810-4
; Sequence 4, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-672-810-4

```

```

Query Match 59.8%; Score 2441; DB 4; Length 1283;
Best Local Similarity 56.4%; Pred. No. 2.7e-229;
Matches 465; Conservative 168; Mismatches 174; Indels 18; Gaps 5;

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Qy 2 VDENDIRALNVRTHRDHGVTSQBPVLFGTISNNIKYGRDDVTDDEMERARANAYDP 61
Db 456 VDGQDRTINVRFLREIIGVTSQBPVLFGTISNNIKYGRDDVTDDEMERARANAYDP 515
Qy 62 IMEFPNKENTLVGEGKQMSGQKQRIALARALVQPHILLDEATSDNDSEKVVQAA 121
Db 516 IMKLPQKEDTLVGERGALSGGQKQRIALARALVQPHILLDEATSDNDSEKVVQAA 575
Qy 122 LEKASKGRTTIVAHRLSTVRNADVIAGDDGVIVVEKGNHDELMKEKGIYFLVMTQTAG 180

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Db 576 LOKARKGRTTIVAHRLSTVRNADVIAGDDGVIVVEKGNHDELMKEKGIYFLVMTQTAG 635
Qy 181 -----KKADE---QMSMTYSTERTKNSL-----PLHSVKSIKSDFDIKABESTOSKEI 226
Db 636 NEIETLENAADESKSEIDTLEMSHDSGSLIRKSTRRSVRSGSQG--DRKLSLKEALDE 693
Qy 227 SLPEVSLILKILKPKDEPFWLGLTILASVLNGCTVHPVPSIIIPAKLIITMF-GNNDKTTLKH 285
Db 694 SIPPVSFWIMKMLNLTENFYFVGVCFAIINGLQPAFAVIFSKLIGITRNDDAETKQ 753
Qy 286 DABIVSMIFVLGIVCFVFMQGLFYGRAGBILTNRLHLAFKAVLYODIAWFDEKENS 345
Db 754 NSNLSLLFLVLGIVSFTTFLQGFPGKAGEIILTKRLRYMVFMSMLRQDVSNFDDPKNT 813
Qy 346 TGGTTLTILADIAIOGATSGRIGVLTQNTATNMGSLVIIISFYGEMTFLILSIAPVLAV 405
Db 814 TGAITRILANDAAQVKGAIKSLRLAIITQNTANLGTGIIISLVGQTLTLLLAIVPIIAL 873
Qy 406 TGMTETAMTGFANKQBLKHAQKIATEALENIRTVSLTRKAFQMYEEMLOTOHRN 465
Db 874 AGVYEMXLSQALUKDKLEGAGKIATEAIENFRITVVSUTQEQKFPHMYDQSLQVPYRN 933
Qy 466 TSKAQIIGSCYAFSHAFIYFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 525
Db 934 SLRKAHIFGITFTQAMMYFAYAGFRFGAYLVAHSLMSFEDVLLVFSAVFGAMAVGQ 993
Qy 526 TLVLAPYSKAKSAAHLFALLEKKPNIDSRQKGPDTCEGNLBRFVSFFYPCRPDV 585
Db 994 VSSPAPDYAKAKVSAHHIIMIEKTPLDISTYSTGLKPNTEGNTFNEVFNYPTRLDI 1053
Qy 586 FILGSLISIERGKTVAFFVSGSGGKSTVOLLORLYDPVQGVLDGDAKELAVOWLR 645
Db 1054 PVLQGLSLEVKKGQTLALVSGSGGKSTVOLLBRFYDPLAGKVLLOGKEIKQLNVQWLR 1113
Qy 646 SOIAIVPOBPVLPNCSTAEINAYGNSRWVFLDBIKAAANAANTHSFIEGLPEKINTQVG 705
Db 1114 AHLGIVSQEPILFDCSISEINAYGNSRWVSEIIVRAAKEANIHAFIESLPNKYSTRVG 1173
Qy 706 LKGAQLSGGQKQRIALARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 765
Db 1174 DKGTLQSGGQKQRIALARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 1233
Qy 766 THRLSAIQNADLIVVFNQGRVKEHGTQQLLAQKGIYFSMVVQA 810
Db 1234 AHRSTIQNADLIVVFNQGRVKEHGTQQLLAQKGIYFSMVVQA 1278

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RESULT 3

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US-09-672-810-7
; Sequence 7, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-810-7

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Query Match 59.8%; Score 2438; DB 4; Length 1280;
Best Local Similarity 56.8%; Pred. No. 5.2e-229;

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Matches 467; Conservative 162; Mismatches 178; Indels 18; Gaps 4;

QY 2 VDENDRALNVRHVRDHIGVWSQEPVLFGTTISNNIKYGRDDVTDEMERARANAAYDF 61
Db IDQDQRTINVRHRLRITGVVSGEPVLFGTTIAENIRYGRNVTDIEIKAVKEANAYDF 513
QY 62 IMEFPNKNFTLVGKGAQSGGOKORIAARALVRNPVKILILDEATSDLSKSAVQAA 121
Db IMKLPNKFDTLVGKGAQSGGOKORIAARALVRNPVKILILDEATSDLSKSAVQAA 573
QY 122 LEVASKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAEALMAKRGYLYSLVMSQ 181
Db LDKARKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAEALMAKRGYLYSLVMSQ 571
QY 182 KADEQMESMTYSTERTNSLPLHSVKSIDSDEI-----DKABESTQSKI 226
Db GNEIENATGESKSSDALEM-SPDSSGLIKRSTRSHPAQQDQKLGKTKEDLNE 691
QY 227 SLPEVLLKILKLNKPEWPFVLTGLASVLNGTVHPVFSIIFAKIIITMP-GNNDKTTLKH 285
Db NVPSSVFWRLKLNSTWPFVVGIFCAIINGGLQPAFAIIFERIIGITRDEDPETKQ 751
QY 286 DAIYSMIFVLGVI CFVSFVMGGLFYGRAGEILTMRHLRHLAKMAYODIAWDEKENS 345
Db NSNMFVFLVGLIISFITFLQGFYGRAGEILTMRHLRHLAKMAYODIAWDEKENS 811
QY 346 TGGTTLAIDIAIQIAGATGSRICVLTQNTNMGSLVSIISFYGWEMTFLILSIAPLAV 405
Db TGTALTRLANDAQQVKAIGSLRAVITQNIANGTGIISLIYVQWLTLLLAIVPIIAL 871
QY 406 TGMETAMTGFANKQKQELKHAGKIATBALENIRITVSLTRKATPEQWYEMLOTHRN 465
Db AGVEMKMLSGQALDKKKELEGAGKIATBALENIRITVSLTRKATPEQWYEMLOTHRN 931
QY 466 TSKAQIIGSCYAFSAFIYFAAAGFRFGAYLIQAGRWTPGCMFIVTFAIAYGAMAIGK 525
Db SLKAMIFGVSPITQWMTYFAGCFRFGAYLVANEFMFDVLVFSALVFGANAVQ 991
QY 526 TLVLAPEYSKAGGAHLFALLEKKNIDRSQEGKKPOTCEGNLFREVSFFYPCRPDV 585
Db VSSFAPDYAKARVSAAHVIMIEKSLIDSYSPHGLKPNLTGNTVFNVEVFNPTREDI 1051
QY 586 FILRGLSLTERGKTVAFFVSGSCGKSTVQLLORLYDPVQGVLPDGVDAKELNQMWR 645
Db PVQLGLSLEVKKQTLALVSSCGKSTVQLLORLYDPVQGVLPDGVDAKELNQMWR 1111
QY 646 SQIAIVPQEPVLFNCISIAENIAYGDSRVVPLDEIKEAANAANIHSFIEGLPEKNTQVG 705
Db AHLGIVSQEPILFDCSIAENIAYGDSRVVSHHEIIMQAAKEANIHFIEITLPEKNTQVG 1171
QY 706 LKGAQISGGOKORIAARALOKPKILILDEATSDLSKSAVQAA 765
Db DKGTQLSGGOKORIAARALVQPHILLDEATSDLSKSAVQAA 1231
QY 766 THRISAQONADLTIVLHNGIKKQGTQHEILLNRDIYFKLVNAQS 810
Db ARLSTIQNADLTIVVQNGVKEHGTQQLAOKGIYFSMISVQA 1276

RESULT 4
US-08-784-649A-2
; Sequence 2, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Siskic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park

STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg. No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1279 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-784-649A-2

Query Match 59.7%; Score 2436; DB 2; Length 1279;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;

QY 2 VDENDRALNVRHVRDHIGVWSQEPVLFGTTISNNIKYGRDDVTDEMERARANAAYDF 61
Db IDQDQRTINVRHRLRITGVVSGEPVLFGTTIAENIRYGRNVTDIEIKAVKEANAYDF 511
QY 62 IMEFPNKNFTLVGKGAQSGGOKORIAARALVRNPVKILILDEATSDLSKSAVQAA 121
Db IMKLPNKFDTLVGKGAQSGGOKORIAARALVRNPVKILILDEATSDLSKSAVQAA 571
QY 122 LEVASKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAEALMAKRGYLYSLVMSQ 178
Db LDKARKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAEALMAKRGYLYSLVMSQ 631
QY 179 ---DIKKADEQMESMTYSTERTNSLPLHSV-----KSIK-SDFIDKABESTQSKLSL 228
Db NEVELENADESKSIDALEMSNDSSRLKRGSTRSVSGSQADRLSKTKEALDESI 691
QY 229 PEVSLKILKLNKPEWPFVLTGLASVLNGTVHPVFSIIFAKIIITMPGN-NDKTTLKHDA 287
Db PPVSFWRIMKLNLTWPFVVGVCALINGGLQPAFAIIFSKLIIGVTRIDDPETKQNS 751
QY 286 EYYSMIFVLGVI CFVSFVMGGLFYGRAGEILTMRHLRHLAKMAYODIAWDEKENS 347
Db NLFSLPLALGIIISFITFLQGFYGRAGEILTMRHLRHLAKMAYODIAWDEKENS 811
QY 348 GTTTLAIDIAIQIAGATGSRICVLTQNTNMGSLVSIISFYGWEMTFLILSIAPLAVTG 407
Db ALTTRLANDAQQVKAIGSLRAVITQNIANGTGIISLIYVQWLTLLLAIVPIIAL 871
QY 408 MIETAAMTGFANKQKQELKHAGKIATBALENIRITVSLTRKATPEQWYEMLOTHRN 467
Db VVEMKMLSGQALDKKKELEGAGKIATBALENIRITVSLTRKATPEQWYEMLOTHRN 931
QY 468 KKAQIIGSCYAFSAFIYFAAAGFRFGAYLIQAGRWTPGCMFIVTFAIAYGAMAIGKT 527
Db RKAHIFGTFITQWMTYFAGCFRFGAYLVANEFMFDVLVFSALVFGANAVQ 991
QY 528 VLAPEYSKAGGAHLFALLEKKNIDRSQEGKKPOTCEGNLFREVSFFYPCRPDVFI 587
Db SPAPDYAKARVSAAHVIMIEKSLIDSYSPEGLMNTLEGNVTGEVFNVEVFNPTREDI 1051
QY 588 LRLGLSLTERGKTVAFFVSGSCGKSTVQLLORLYDPVQGVLPDGVDAKELNQMWR 647

Db 1052 LQGLSLEVKGGTALVGGSGGKSTVQLLRFYDPLAGVLDGKEIKELNVQWURAH 1111
Qy 648 IAIPOEPVLFNCISAEIAENIAYGDSRVVPLDEIKEAANAANIHSFIEGLPEKNTVOGLK 707
Db 1112 LGIVSQEPILFDCSIAENIAYGDSRVVSQEIIVRAAKBANIHAFTESLPKYSTKVGDK 1171
Qy 708 GAOLSGGQKORLAIALARALLQKPKILLDDEATSDNDSEKVVQCHALDKARTGRCIVIAH 767
Db 1172 GTQLSGGQKORLAIALARALVRQPHILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 1231
Qy 768 RLSAIONADLIIVLHNGKIKQOQTHQELLNRDIYFKLVNAQS 810
Db 1232 RLSTIQNADLIIVFQNGRVKHEGTHQOLLAQKGIYFVSWSVQA 1274
RESULT 5
US-09-672-810-6
; Sequence 6, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-810-6
Query Match 59.7%; Score 2436; DB 4; Length 1279;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
Qy 2 VDENDIRALNVRHYRDHIGVWSQEPVLFQTTISNNIKYGRDDVTDDEMERAAEANYDF 61
Db 452 VGGQDRTINVRLEIRIIGVWSQEPVLFATTAENIRYGRENVMTDEIKAVKEANYDF 511
Qy 62 IMEPFNKENTLVGKGAQMSGQKORLAIALARALVRNPKILLDDEATSDNDSEKSAVQAA 121
Db 512 IMKLPKHFDTLVGERGAGLSSGQKORLAIALARALVRNPKILLDDEATSDNDSEKSAVQAA 571
Qy 122 LEKASKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKGAHAELMAKRGLYYSVMSQ--- 178
Db 572 LDKARKGRTTIVIAHRLSTVRNADVIAGFDGVIKEGNHDELAKKEGIVFKLVMTQTAG 631
Qy 179 ---DIKKADEQMSMTYSTERTKNSLPLHSV-----KSIIK-SDFIDKAEESTOSKEISL 228
Db 632 NEVELENADESKSEIDALEMSNDSSRLIRKSTRSVGSQAQRKLSKEALDESI 691
Qy 229 PEVSLKLIKLNKPEWPFVLGTLASVNGTVHVFVSTIIPAKIITMFGN-NDKTTLKXDA 287
Db 692 PVSFWIRMKLNTWPFVGVPCAIINGLQPAFALIPSKIIIGVFTRIIDDPETKQNS 751
Qy 288 EYISMIFVLGVICVSVPMOGLFVRAGETILTWELRLHAKMLYODIAMFOKENSTG 347
Db 752 NULFSULFALGLIISITITFLOQFTPKAGEILTKELRVNFRSMRLQDVSWFDPKNTG 811
Qy 348 GLTTILAIIDIAIQGATSGRIGVLTQNTATNMGSLVSIISFYIGWENTFILLSIAPLAVTG 407
Db 812 ALTTFLANDAAQVKGAIGSRLAVITQNTIANLGTGIIISFYIGWQTLTLLAIVPIIAIAG 871
Qy 408 MIETAMTGFANKDQELKHAKGIAATEALENIRITVSLTREKAFQMYEMLQOHRNTS 467

Db 872 VDEMRLSQAULKKEKELSGAGKIATEAENFRVVSLSLTQEQKFEHMYAQSLQVPRNSL 931
Qy 468 KKAQIIGSCYAFSHAFIYFAYAGFFGAYLIQAGRMTPGGMFIYFTAIYAGMAIGKTL 527
Db 932 RKAHIFGITTSFTQAMWYSYAGCFRFGAYLVAHKLMSFEDVLLVFSAVVFGAMAVQVS 991
Qy 528 VLAPEYSKAKSNAHLFALLEKKNIDSRQKPKDTCBGNLEFRFVFYPCRDVFI 587
Db 992 SPAPDFAKAKISAHHIIMIEIKTFLDYSYSTGLMPTLEGNTVFGVFNFTRPDIPV 1051
Qy 588 LRGLSLSIRBKTVAFVSGSGGCKSTSVQLLQRLYDVPQOVLFDGVDKAKELNVQWURAH 647
Db 1052 LQGLSLEVKGGTALVGGSGGKSTVQLLRFYDPLAGVLDGKEIKELNVQWURAH 1111
Qy 648 IAIPOEPVLFNCISAEIAENIAYGDSRVVPLDEIKEAANAANIHSFIEGLPEKNTVOGLK 707
Db 1112 LGIVSQEPILFDCSIAENIAYGDSRVVSQEIIVRAAKBANIHAFTESLPKYSTKVGDK 1171
Qy 708 GAOLSGGQKORLAIALARALLQKPKILLDDEATSDNDSEKVVQCHALDKARTGRCIVIAH 767
Db 1172 GTQLSGGQKORLAIALARALVRQPHILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 1231
Qy 768 RLSAIONADLIIVLHNGKIKQOQTHQELLNRDIYFKLVNAQS 810
Db 1232 RLSTIQNADLIIVFQNGRVKHEGTHQOLLAQKGIYFVSWSVQA 1274
RESULT 6
US-09-767-594-2
; Sequence 2, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives
; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human p-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
US-09-767-594-2
Query Match 59.7%; Score 2436; DB 4; Length 1280;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
Qy 2 VDENDIRALNVRHYRDHIGVWSQEPVLFQTTISNNIKYGRDDVTDDEMERAAEANYDF 61
Db 453 VGGQDRTINVRLEIRIIGVWSQEPVLFATTAENIRYGRENVMTDEIKAVKEANYDF 512
Qy 62 IMEPFNKENTLVGKGAQMSGQKORLAIALARALVRNPKILLDDEATSDNDSEKSAVQAA 121
Db 513 IMKLPKHFDTLVGERGAGLSSGQKORLAIALARALVRNPKILLDDEATSDNDSEKSAVQAA 572
Qy 122 LEKASKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKGAHAELMAKRGLYYSVMSQ--- 178
Db 573 LDKARKGRTTIVIAHRLSTVRNADVIAGFDGVIKEGNHDELAKKEGIVFKLVMTQTAG 632
Qy 179 ---DIKKADEQMSMTYSTERTKNSLPLHSV-----KSIIK-SDFIDKAEESTOSKEISL 228

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Db 633 NEVELENADESKESDALEMSNDSSRLKRSTRSRVSGSOAQDRKLSKTEALDESI 692
Qy 229 PEVSLKILKLNKPEMPFVVLGTLASVNGTVHPVFSIIIPAKIITMFGN-NDKXITLKHDA 287
Db 693 PPVSFWRIKMLNLTWPYFVGVFCALINGGLQAPAFIIFSKLIIGVTRIDDPETKQNS 752
Qy 288 ELYSMIEVLGIVCFVSFVMOGLFYGRAGEILTWRLHLPKAMLYQDIWAFDEKENSIG 347
Db 753 NLFSLFLAUGIISFIFLQGTGKAGELITKRLRYMFRSMRLQDVSFDDPKMTTG 812
Qy 348 GLTTLAIDIAIQGATGSRIGVLTQATNMGSLVSIISFYIGWMTFLILSIAPVLAVTG 407
Db 813 ALTRLANDAAQVKAIGSLAVITQNIANGTGIIISFYIGWLTLLLLAIIVPIAIAG 872
Qy 408 MIETAAMTGPANKQKQELKAGKIATEALENITIVSLTREKAFQMYEMLQTOHRNYS 467
Db 873 VWMKMLSGQALKKQKLEGAAGIATEAIEENFRVTVSLTQEQKFHMYAQSLQVPRNSL 932
Qy 468 KKAQIIGSCVAFSHAFIYFAYAGFRFGAYLIQAGRWTPGEMIFVFTAIYAGAMAIGKTL 527
Db 933 KKAHIFGIFTSFTQAMMYFSYAGCFRFGAYLVAKMLSPEDVLLVFSVAVFGMAVGQVS 992
Qy 528 VLAPEYSKAKSGAAHLPALLEKXPNIDSRQSGKDPDTCGNLEPREVFFYPYCRDPVFI 587
Db 993 SPAPDYAKAKISAAHIIMITEKFLIDSYSYTEGLMPNTEGNTFGEVVFYTRPDIPV 1052
Qy 588 LRGLSLIERGKTVAFCVSSGCKSTSVOLLQRLYDPVGOVLFDGVDAKELNVQWLRSQ 647
Db 1053 LQGLSLVKKQGTALVVGSGCGKSTVQLLEFYDPLAGKVLDDGKEIKRLNVQWLRH 1112
Qy 648 IALVQEPVLFNCISAEINAYGDNRSRVPLDEIKEAANAANIHSFIEGLPKYNTQVGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAKEANIHFIESLPNKYSTKVGDK 1172
Qy 708 GAOLSGGOKORLAIARALLOKPKILLDEATSALENDSEKVVQHALDKARTGRTCLVVT 767
Db 1173 GTQLSGGOKORLAIARALVROPHILLDEATSALENDSEKVVQHALDKAREGRTCIIVAH 1232
Qy 768 RLSAIONADLIIVLHNGKIKEQGTQHELLNRDIYFKLVNAQS 810
Db 1233 RLSTIQNADLIIVFQNGRKEHGHGTHQQLAQKGIYFSMVVQA 1275
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RESULT 7

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US-09-672-810-5
; Sequence 5, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-810-5
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Query Match 59.7%; Score 2436; DB 4; Length 1280;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
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Qy 2 VBENDIRALNVRHYRDHIGVWSQSPVLFGTTISNNIKYGRDDVTDSEVRAAEANAYDF 61
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Db 453 VDGQDIRTINVRPLSEIIGVWSQEPVLFATTIAENIRYGRNVTWDEIKAYKEANAYDF 512
Qy 62 IMEFPKNTLVGEGKAGQSGOKQRIARALVARNPKILILDEATSALEDSKSAVQAA 121
Db 513 INKLPKPDVLGVRGAQLSGOKQRIARALVARNPKILILDEATSALEDSKSAVQAA 572
Qy 122 LEKASGRITIVVAHRLSTIRSDILVTLKOGKABKAGAHLEMAKRGYIYSLVMSQ--- 178
Db 573 LDKAEKGRITIVIAHRLSTIRSDILVTLKOGKABKAGAHLEMAKRGYIYSLVMSQ--- 632
Qy 179 ---DIKKADBOEMESMTYSTERTKINSPLHVS-----KSIK-SDFIDKAEESTOSKELSL 228
Db 633 NEVELENADESKESDALEMSNDSSRLKRSTRSRVSGSOAQDRKLSKTEALDESI 692
Qy 229 PEVSLKILKLNKPEMPFVVLGTLASVNGTVHPVFSIIIPAKIITMFGN-NDKXITLKHDA 287
Db 693 PPVSFWRIKMLNLTWPYFVGVFCALINGGLQAPAFIIFSKLIIGVTRIDDPETKQNS 752
Qy 288 ELYSMIEVLGIVCFVSFVMOGLFYGRAGEILTWRLHLPKAMLYQDIWAFDEKENSIG 347
Db 753 NLFSLFLAUGIISFIFLQGTGKAGELITKRLRYMFRSMRLQDVSFDDPKMTTG 812
Qy 348 GLTTLAIDIAIQGATGSRIGVLTQATNMGSLVSIISFYIGWMTFLILSIAPVLAVTG 407
Db 813 ALTRLANDAAQVKAIGSLAVITQNIANGTGIIISFYIGWLTLLLLAIIVPIAIAG 872
Qy 408 MIETAAMTGPANKQKQELKAGKIATEALENITIVSLTREKAFQMYEMLQTOHRNYS 467
Db 873 VWMKMLSGQALKKQKLEGAAGIATEAIEENFRVTVSLTQEQKFHMYAQSLQVPRNSL 932
Qy 468 KKAQIIGSCVAFSHAFIYFAYAGFRFGAYLIQAGRWTPGEMIFVFTAIYAGAMAIGKTL 527
Db 933 KKAHIFGIFTSFTQAMMYFSYAGCFRFGAYLVAKMLSPEDVLLVFSVAVFGMAVGQVS 992
Qy 528 VLAPEYSKAKSGAAHLPALLEKXPNIDSRQSGKDPDTCGNLEPREVFFYPYCRDPVFI 587
Db 993 SPAPDYAKAKISAAHIIMITEKFLIDSYSYTEGLMPNTEGNTFGEVVFYTRPDIPV 1052
Qy 588 LRGLSLIERGKTVAFCVSSGCKSTSVOLLQRLYDPVGOVLFDGVDAKELNVQWLRSQ 647
Db 1053 LQGLSLVKKQGTALVVGSGCGKSTVQLLEFYDPLAGKVLDDGKEIKRLNVQWLRH 1112
Qy 648 IALVQEPVLFNCISAEINAYGDNRSRVPLDEIKEAANAANIHSFIEGLPKYNTQVGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAKEANIHFIESLPNKYSTKVGDK 1172
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Db 1173 GTQLSGGOKORLAIARALVROPHILLDEATSALENDSEKVVQHALDKAREGRTCIIVAH 1232
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Db 1233 RLSTIQNADLIIVFQNGRKEHGHGTHQQLAQKGIYFSMVVQA 1275
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RESULT 8

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5206352-4
; Patent No. 5206352
; APPLICANT: Robinson, Igor B.;Pastan Ira H.;Gottesman, Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO:4;
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LENGTH: 1280

TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DNA V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-583-276-19

Query Match 59.7%; Score 2436; DB 2; Length 1280;
Best Local Similarity 56.6%; Pred. No. 1.3e-228;
Matches 466; Conservative 165; Mismatches 178; Indels 14; Gaps 4;

Qy 2 VDENDIRALNVRHYRHDHIGVWSQEPVLPGTTISNNIKYGRDDVTDDEMERAAENAYDF 61
Db 453 VDQDQIRTNVRFLEIIGVWSQEPVLPGTTISNNIKYGRDDVTDDEMERAAENAYDF 512
Qy 62 IMEPFNKNTLVGKGAQSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 121
Db 513 IMKLPKHFDTLVGERAQLSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 572
Qy 122 LEKASKGRTTIVVAHRLSTIRSDLVTLKQGLMAEKGAHAELMAKRGLYSLVMQ--- 178
Db 573 LDKARKGRTTIVIAHRLSTVRNADVIAGDDGVIVKGNHDELMKEKGIYFKLVTMTAG 632
Qy 179 ---DIKKADQEMESMTYSTERTKNSLPLHSV-----KSIK-SDFIDKABEESTQSEISL 228
Db 633 NEVELENAADESKSHIDALEMSNDSSRLIRKSTRSVRGSAQDRKLSKTEALDESI 692
Qy 229 PEVSLKILKLNKPEPFPVVLGTLASVLNGTVPVPSIIIPAKIITMFGN-NDKTTLKHDA 287
Db 693 PPVSPWRIMKLNLTENPYPVWGVFCALINGGLQPAFALIFSKIIGVFTRIDDPETKQNS 752
Qy 288 EIVSMIPVILGVICFVSFMOGLFYGRAGEILTMRLHRLAPKAMLYODIAWFEKENSTG 347
Db 753 NLFSLLFALGIIISPIITFLOGETFGKAGEILTKRLRYMVRSMRLQDVSFDDPKNTTG 812
Qy 348 GLTTILADIAIQGATGSRIGVLTQNTATNGLSVIIISFYIYGMETPLILISAPVLAVTG 407
Db 813 ALITRLANDAAQVKGAGISRLAVITQNIANLGTGIIISFYIYGMETPLILISAPVLAVTG 872
Qy 408 MIETAAMTGPAKDKOELKHAQKIAATEAENITIVSLREKAFECOMYEMLOTHRENTS 467
Db 873 VWEKMLSGQALKDKKELEBAGKIAATEAENITIVSLREKAFECOMYEMLOTHRENTS 932
Qy 468 KKAQILGSCYAFSHAFIYFAYAAAGFRFGAYLIQAGRWMTPEGMFIVFTAYAGMAIGKTL 527

Qy 2 VDENDIRALNVRHYRHDHIGVWSQEPVLPGTTISNNIKYGRDDVTDDEMERAAENAYDF 61
Db 453 VDQDQIRTNVRFLEIIGVWSQEPVLPGTTISNNIKYGRDDVTDDEMERAAENAYDF 512
Qy 62 IMEPFNKNTLVGKGAQSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 121
Db 513 IMKLPKHFDTLVGERAQLSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 572
Qy 122 LEKASKGRTTIVVAHRLSTIRSDLVTLKQGLMAEKGAHAELMAKRGLYSLVMQ--- 178
Db 573 LDKARKGRTTIVIAHRLSTVRNADVIAGDDGVIVKGNHDELMKEKGIYFKLVTMTAG 632
Qy 179 ---DIKKADQEMESMTYSTERTKNSLPLHSV-----KSIK-SDFIDKABEESTQSEISL 228
Db 633 NEVELENAADESKSHIDALEMSNDSSRLIRKSTRSVRGSAQDRKLSKTEALDESI 692
Qy 229 PEVSLKILKLNKPEPFPVVLGTLASVLNGTVPVPSIIIPAKIITMFGN-NDKTTLKHDA 287
Db 693 PPVSPWRIMKLNLTENPYPVWGVFCALINGGLQPAFALIFSKIIGVFTRIDDPETKQNS 752
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Db 753 NLFSLLFALGIIISPIITFLOGETFGKAGEILTKRLRYMVRSMRLQDVSFDDPKNTTG 812
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Db 813 ALITRLANDAAQVKGAGISRLAVITQNIANLGTGIIISFYIYGMETPLILISAPVLAVTG 872
Qy 408 MIETAAMTGPAKDKOELKHAQKIAATEAENITIVSLREKAFECOMYEMLOTHRENTS 467
Db 873 VWEKMLSGQALKDKKELEBAGKIAATEAENITIVSLREKAFECOMYEMLOTHRENTS 932
Qy 468 KKAQILGSCYAFSHAFIYFAYAAAGFRFGAYLIQAGRWMTPEGMFIVFTAYAGMAIGKTL 527
Db 933 RKAHIFGTTFTQAMTTFVSAGCFRFGAYLVAKHLMSEFEDVLLVFSAVVFGMAVQVS 992
Qy 528 VLAPKSKAGSAHLFALLEKKNIDSRQEKKPDCEGNLSFRVSFPCBPVFI 587
Db 993 SFAPDYAKAKISAHHIMIIKTPIDISYSTEGLMPTLEGNVTFGEVFNPIRDPV 1052
Qy 588 LRGLSLIERGKTVAFVSSGCGKSTSVQLLQRLYDVPVQGVLPDGVDAKELNVQLRSQ 647
Db 1053 LQGLSLVKKGTALVSSGCGKSTSVQLLQRLYDVPVQGVLPDGVDAKELNVQLRSQ 1112
Qy 648 LAIVDQEPVLPNCSTAEINAYGDSRVVPLDEIKEAANAHHISFIEGLPEKNTVGLK 707
Db 1113 LGIVSQEPILFDCSTAEINAYGDSRVVQBEIVRAAKEANIHAIFISLPNKYSTKYGDK 1172
Qy 708 GAQLSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 810
Db 1173 GTQLSGGQKQRIARALVRNPKILLDEATSALESSEKSAVQAA 1232
Qy 768 RLSTQNLADLIIVFNGRVRKHGTQQLLAQKGIYFSMVVQA 1275
Db 1233 RLSTQNLADLIIVFNGRVRKHGTQQLLAQKGIYFSMVVQA 1275

RESULT 9
US-08-583-276-19
Sequence 19, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolcoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN

Db 933 RKAHIFGTFSTQAMMYFAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMVGVQS 992
 QY 528 VLAPYSKAKSGAHLFALEKXPNIDSRSGKPKDTCGNLEFREVSVFFYPCRPDVEI 587
 Db 993 SFAPDAKAKISAHIMIEKPLDIDSYSFEGMLNTLEGNTFGEVNVYTRDIPW 1052
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 QY 648 IATVQEPVLPNCSIAENIAYGNSRVVPLDEIKEAANAANIHSFTEGLPEKYNTOVGLK 707
 Db 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQEEIVRAKEANIHAFIESPNKISTKVGDK 1172
 QY 708 GAQLSGGQKQRIARALLOKPKILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 767
 Db 1173 GTQLSGGQKQRIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 1232
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RESULT 10

US-09-120-513-2
 ; Sequence 2, Application US/09120513
 ; Patent No. 6025160
 ; GENERAL INFORMATION:
 ; APPLICANT: Brum, Kimberly
 ; APPLICANT: Chenery, Richard
 ; APPLICANT: Ellens, Harma
 ; APPLICANT: Field, John
 ; APPLICANT: Yue, Lin
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
 ; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDR1B2 AND
 ; TITLE OF INVENTION: SCREENING METHODS THEREOF
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Smithline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/120.513
 ; FILING DATE: 22-JUL-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: King, William T
 ; REGISTRATION NUMBER: 30,954
 ; REFERENCE/DOCKET NUMBER: GP50008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5015
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-120-513-2

Query Match 59.2%; Score 2413.5; DB 3; Length 1275;
 Best Local Similarity 56.8%; Pred. No. 1.3e-226;
 Matches 467; Conservative 158; Mismatches 180; Indels 17; Gaps 5;

QY 2 VDENDIRALNVHRDHIQVWSQBPVLFCTTISNNIKYGRDDVDVDEEMRAAREANAYDF 61
 Db 451 IDQDITINRYLREILIGVWSQBPVLFCTTISNNIKYGRDDVDVDEEMRAAREANAYDF 510
 QY 62 INEPKNTLVGKGAQWQSGGQKQRIARALVNPXKILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 121
 Db 511 IMKLPHKNTLVGKGAQWQSGGQKQRIARALVNPXKILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 570
 QY 122 LKASKGRITTVVVAHRLSTIRSDLVTLKDGMLAEKGAHAEKMAKRGYLYSLVMSQDITK 181
 Db 571 LKAREGRITTVIAHRLSTIRSDLVTLKDGMLAEKGAHAEKMAKRGYLYSLVMSQDITK 629
 QY 182 KADEQESMSTYTERKTNLSPLHSVKSIDSFDKA-----BESTOSKE---IS 227
 Db 630 GNEIPEGNNAYESQSDTGASELTSEKS-KSPILRIRRSIHRRODQERRLSKEDVDD 688
 QY 228 LPEVSLKILKLNKPEWPFVVLGTSLASVLTGTVHVPFSIIFAKIITMFC-NNDKITLKH 286
 Db 689 VPMVSPWQLKLNISEMPVVLVGVLCVINGCIQVFAIVPSKIVGVPSRDDDDHETKQKN 748
 QY 287 ABIYSMIFVLGVICFVSFMQGLFYGRAGEILTWRHLHLAFKAMLYQDIADHEKENST 346
 Db 749 CNLFSLLFLVMGMISEFVTFPGQKAGEILTWRHLHLAFKAMLYQDIADHEKENST 808
 QY 347 GGLTTILAJDIAQIGATSGRIGVLTONTNMGSLVSIISPIYQWEMTFLILSIAPVLAVT 406
 Db 809 GGLTTILASDASNVKSGSLAVTVQNVANLGTGILSLVYQWLTLLVILVILVILG 868
 QY 407 GMIETAAMTFPANKQKQELKHAKIATEALENIRITVSLTRKAPQOMTEMLQTHRNT 466
 Db 869 GIIEMKLLSQALKDKKKELEISKIATEAIENFRTVSLTREKQFETMYAQSILQIPYRNA 928
 QY 467 SKKAQIIGSCYAFSAFIYFAYAAAGFRFGAYLIQAGRMTPGEMFIYFTALAYGAMAIGKT 526
 Db 929 LKARHVFGITPAFTQMIYFSAACFRFGAYLVARELMTFENVVLFSAVVGAMAGNT 988
 QY 527 LVLAPYSKAKSGAHLFALEKXPNIDSRSGKPKDTCGNLEFREVSVFFYPCRPDVEI 586
 Db 989 SSPADYAKAKVSASHIIRIEKIPEIDSYSTGLKPNWLGKNGVNFYPTSPNIP 1048
 QY 587 ILRLSLSIERGKTVAFVGGSGGKSTVQLLQRLYDPVQGVLFQGVDAKELNVQMLRS 646
 Db 1049 VLOGLSFEVKKGQTLALVGGSGGKSTVQLLQRLYDPVQGVLFQGVDAKELNVQMLRS 1108
 QY 647 QIAIVPQEPVLPNCSIAENIAYGNSRVVPLDEIKEAANAANIHSFTEGLPEKYNTOVGL 706
 Db 1109 HLGVSQEPILFDCSITENIAYGNSRVVSHHEIVRAKEANIHQFIDSLPEKYNTRVGD 1168
 QY 707 KGAQLSGGQKQRIARALLOKPKILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 766
 Db 1169 KGTQLSGGQKQRIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLVWTH 1228
 QY 767 HRLSAIQNADLIIVLHNGKIYKQTHQELINRDIYFKLVNA 808
 Db 1229 HRLSTIQNADLIIVFQNGRVKHEGTHQQLAQKGIYFSWVQQA 1270

RESULT 11

US-09-450-105-2
 ; Sequence 2, Application US/09450105
 ; Patent No. 6163166
 ; GENERAL INFORMATION:
 ; APPLICANT: Kimberly Anne Brum
 ; APPLICANT: Richard James Chenery
 ; APPLICANT: Harma Ellens
 ; APPLICANT: John Anthony Feild
 ; APPLICANT: Lin Yue
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
 ; TITLE OF INVENTION: ENCODING RAT MDR1B2 AND SCREENING METHODS THEREOF
 ; FILE REFERENCE: GP-50008-D1
 ; CURRENT APPLICATION NUMBER: US/09/450.105
 ; CURRENT FILING DATE: 1999-11-29

Db 873 VVENKMPAGQALKKDKELEGAGKIATEIAENFRTVSLTQEQKEHMYAQSLOQVYRNSL 932
Qy 468 KKAQIIIGSCYAFSHAFTYFAYAGCFREGAYLIOAGRMTPGEMFIVFTAIAYGAWAIGKTL 527
Db 933 KKAHIFGITSFTQAMMYESYAGCFREGAYLVAHKLNSFEDVLLVFSVAVFGAMAVGQVS 992
Qy 528 VLAPYSKAKSGAHLFALLKPKNDISRSQBGKPDTCGNELEFREVSFFYPCRPDVFI 587
Db 993 SFAPDYAKAKISAHHIIMEKTPLIDSYSTEGMLPNTLEGNTFGEVWFNYFTREDIPV 1052
Qy 588 LRGLSISIERGKTVAFYGGSGGCKSTSVQLLQRLYDPVQGVLFQVDAKELNVOVLRSQ 647
Db 1053 LQGLSLEVKKGQTLALVGGSGGCKSTVQLLEFYPDLACKVLLDGKEIKELNVQWLRH 1112
Qy 648 IAIVPOEPVLNCSIAENIAYGNSRVVPLDETEKEAANAHIHSFIEGLPEKYNTOUGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQSEIIVRAAKEANIHAFTESLPNKYSTVGDK 1172
Qy 708 GAOLSGGQKORIAIARALLQKPKILLDEATSDALDSEKVOHAKDKARTGTCLVVT 767
Db 1173 GTQLSGGQKORIAIARLVRQPHILLDEATSDALDSEKVOHAKDKAREGRTICIVIAH 1232
Qy 768 RLSAIONADLIVLHNGKIKEQGTQOHLNDRDIYFKLVNAQS 810
Db 1233 RLSTIQNADLIVVFQNGRVEKHGTQOHLAQKGIYFSMVSVQA 1275

RESULT 13

US-09-316-167-2
; Sequence 2, Application US/09316167
; Patent No. 6365357
; GENERAL INFORMATION:
; APPLICANT: Mechetner, Eugene
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/316,167
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/752,447
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6365357nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-9808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-316-167-2

Query Match 59.1%; Score 2412; DB 4; Length 1280;
Best Local Similarity 56.1%; Pred. No. 1.8e-226;

Matches 462; Conservative 164; Mismatches 183; Indels 14; Gaps 4;
Qy 2 VDENDIRALNVHRDHIGVVSQEPVLFGTTTNNIKYGGDDVTDDEMERAPAEANAYDF 61
Db 453 VQODIRITNVFLREIIGVVSQEPVLFAITTAENIRYGRENVTDDEISKAVKEANAYDF 512
Qy 62 IMEFPNKNFTLVGERGAQMSGGQKORIAIARALVRNPKILILDEATSDALDSEKSAVQA 121
Db 513 IMKLPHKFTLVGERGAQMSGGQKORIAIARALVRNPKILILDEATSDALDSEKSAVQA 572
Qy 122 LEKASKGRTTIVVHRLSTIRSDILVTLKQMLAEKGAHBLMAKRGYLYSLVMSQ--- 178
Db 573 LOKARKGRTTIVVHRLSTIRSDILVTLKQMLAEKGAHBLMAKRGYLYSLVMSQ--- 632
Qy 179 ---DIKKADEQMESMTYSTERTNLSPLHSV-----KSIKSDFDIKABEST--QSKEISL 228
Db 633 NEVELLENADESKSEIDALEMSSNDSRLIKRSTRSRVSGSQACHRKLSTKEALDESI 692
Qy 229 PVSULLKILKLNKPPFPVLTGLASLVNGTVHPVPSIFAKIITMFGN-NKDTILKHA 287
Db 693 PVSFWIRMKLNLTEPVPVWGVFCAIINGGLQPAFAIFSKIIIGVFTRIDDPETKQNS 752
Qy 288 EYYSIMFIVLGVICFVSVMQGLFYGRAGEILTMRLHLAFKAMLYQDIAWFEKENSTG 347
Db 753 NLFSLLELALGIIISITFLQSTFGKAGEILTKELRYMFRSMLRQDVSWEHDPKNTTG 812
Qy 348 GLUTTILADIAIQIGATSGRIGVLTONATNMGSLVSIISFYGEMTFELISLAPLVATG 407
Db 813 ALTTRLANDAAQVGAIGSLAVITONTANLGTGIIISFYGQTLTLLLAIVPIATAG 872
Qy 408 MIETAAMTGFANKQKQELKHAGKIATEALENIRTVSLTREKAPFOMYEMLOTOHRNTS 467
Db 873 VVENKMPAGQALKKDKELEGAGKIATEIAENFRTVSLTQEQKEHMYAQSLOVYRNSL 932
Qy 468 KKAQIIIGSCYAFSHAFTYFAYAGCFREGAYLIOAGRMTPGEMFIVFTAIAYGAWAIGKTL 527
Db 933 KKAHIFGITSFTQAMMYESYAGCFREGAYLVAHKLNSFEDVLLVFSVAVFGAMAVGQVS 992
Qy 528 VLAPYSKAKSGAHLFALLKPKNDISRSQBGKPDTCGNELEFREVSFFYPCRPDVFI 587
Db 993 SFAPDYAKAKISAHHIIMEKTPLIDSYSTEGMLPNTLEGNTFGEVWFNYFTREDIPV 1052
Qy 588 LRGLSISIERGKTVAFYGGSGGCKSTSVQLLQRLYDPVQGVLFQVDAKELNVOVLRSQ 647
Db 1053 LQGLSLEVKKGQTLALVGGSGGCKSTVQLLEFYPDLACKVLLDGKEIKELNVQWLRH 1112
Qy 648 IAIVPOEPVLNCSIAENIAYGNSRVVPLDETEKEAANAHIHSFIEGLPEKYNTOUGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQSEIIVRAAKEANIHAFTESLPNKYSTVGDK 1172
Qy 708 GAOLSGGQKORIAIARALLQKPKILLDEATSDALDSEKVOHAKDKARTGTCLVVT 767
Db 1173 GTQLSGGQKORIAIARLVRQPHILLDEATSDALDSEKVOHAKDKAREGRTICIVIAH 1232
Qy 768 RLSAIONADLIVLHNGKIKEQGTQOHLNDRDIYFKLVNAQS 810
Db 1233 RLSTIQNADLIVVFQNGRVEKHGTQOHLAQKGIYFSMVSVQA 1275

RESULT 14

US-09-397-233-2
; Sequence 2, Application US/09397233
; Patent No. 6630327
; GENERAL INFORMATION:
; APPLICANT: Mechetner, Eugene
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/397,233
; FILING DATE: 16-Sep-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6630327nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-397-233-2

Query Match 59.1%; Score 2412; DB 4; Length 1280;
Best Local Similarity 56.1%; Pred. No. 1.8e-226;
Matches 462; Conservative 164; Mismatches 183; Indels 14; Gaps 4;

QY 2 VDENDIRALNVRHFDHIGVVSQBPVLFGTTISNNIKYGRDDVTDREMERAREANAYDF 61
DB 1113 LGIVSQEPILFDCISAENTAYGDSNRVVSQBPVLFGTTISNNIKYGRDDVTDREMERAREANAYDF 1172
QY 708 GAQLSGGQKQRIALAIARALLOKPKILLDEATGALDNDSEKVVQHALDKARTGRTCLVWTH 767
DB 1173 GTQLSGGQKQRIALAIARALVQPHILLDEATGALDNDSEKVVQHALDKARTGRTCLVWTH 1232
QY 768 RISAIQNADLIIVLHNGKIKBOGTHQELLNRNDIYFKLVNAQS 810
DB 1233 RLSTIQNADLIIVVQNGRVRKEHGTHTQOQLAQRGIYFSMVSVQA 1275

RESULT 15
US-08-996-545-2
; Sequence 2, Application US/08996545
; Patent No. 5928898
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; APPLICANT: de Waard, Maarten A.
; APPLICANT: Peery, Robert B.
; APPLICANT: Andrade, Alan C.
; TITLE OF INVENTION: Multiple Drug Resistance Gene at/d of
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,545
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-11766
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; TELEFAX: 317-276-2763
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-545-2

Query Match 41.4%; Score 1690.5; DB 2; Length 1334;
Best Local Similarity 43.5%; Pred. No. 9e-156;
Matches 366; Conservative 152; Mismatches 293; Indels 31; Gaps 7;

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DB 489 LLDGHDIDLNLRLWRQLQISVQBPVLFGTTISNNIKYGRDDVTDREMERAREANAYDF 548
QY 52 AREANAYDFIMEPPNKENTLVGEKGAQMSGQKQRIALAIARALVQPHILLDEATGALDNDSEKVVQHALDKARTGRTCLVWTH 111
DB 549 AARMAHNDHFDITALEPGETVNVQBPVLFGTTISNNIKYGRDDVTDREMERAREANAYDF 608
QY 112 SSKSAVOAALSKASKGRITIVVAHRLSTIRSDLIIVTKDGMALAEKGAHAEIEMAKRGILY 171
DB 112 SSKSAVOAALSKASKGRITIVVAHRLSTIRSDLIIVTKDGMALAEKGAHAEIEMAKRGILY 171

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Db 609 TKSEGVQALERAASGRITVIAHRLSTIKTAHNTIWLNVNGKIAEQGTHDELVDGRGAY 668
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Db 669 RKLVEACRINEQKAEADADAEADITNADIAKIKTASSASSDLCKPPTIDORTGTHKSV 728
Qy 222 QSKXIS-----LPEVSLKILK-----LNKPEPPFVVLGTLASVNGTVHPVFSIIFAKI 271
Db 729 SSAILSKRPPTTPKYSMTLLKLFVASFNRPEIPYMLIGLVFSLAGGGQPTQAVLYAKA 788
Qy 272 ITWFG--NNDKTTLKHDAEITYSMFVILGVICFVSFMOGLFYGRAGEILTWRLRHLAFK 329
Db 789 ISTLSLPESQYSLRHDAFWSLXFFVVGIIQFITQSTNGAAPAVCSERLIRARSTAFR 848
Qy 330 AMLYQDIAMPDEKENSTGTLTILADIAIQIGATSGRIGVLTONATNMGLSVIISPIYG 389
Db 849 TILRQDIAPFDEKENSTGALTSTETKHLSCVSGVTLGTLILMTSTLGAALIIALAIG 908
Qy 390 WEMTPLLILSTAPVLAVTGMTETAAMTGFANKQKQELKHAGKIATEALENIRITVUSLTREK 449
Db 909 WKUALVCISVVPVLLACGFYRFYMLAQFQSRKSLAYEGSANFACEATSSIRIVASLTRE 968
Qy 450 AFQOMYEMLQTOHRNTSKAKAIIGSCYAPSHAFIYFAYAAAGFRFGAYLIQAGRMTPGCM 509
Db 969 DVWEIYHAQLDAQRTSLISVLSRSLLYASSQALVFFCVAGLGFYGGTLLGHEHYDIFRP 1028
Qy 510 FIVETAIAICAMAIKTLVLAPESYKAKSAAHLFALLEKKKNIDSESQEGKKPDTCEGN 569
Db 1029 FVCFSEILFQAQAGTVFSTAPDMGKAKNAAEFRLEFRKPKPOIDNWSSEGEKLETVGE 1088
Qy 570 LEPREVSFFYPCRPDVFILRGLSLSIERGKTAVFVSGSGCKSTSVQLLQRLYDPVQGV 629
Db 1089 IEFNRVHFRYPTREQPVLRGLDLTVKPGQYVALVSGSGCKSTTALLERFYDAIAGSI 1148
Qy 630 LFGVDAXELNVQWLSQTAIVQEPVLFNCSTAENIAYGDNRSVVPLDEIKEAANAANI 689
Db 1149 LVDGKOISKLININSYRSLVLSVQEPVLYQGTIKENILILGIVEDDVPBFLIKACKDANI 1208
Qy 690 HSTIEGLPEKYNTOVGLKGAQLSGGOKORLAIARALLQKPKILLDEATSAIDNDSEKV 749
Db 1209 YDFIMSLPEGFNTVWSKGMLSGGQKQVARIARALLRDPKILLDEATSAIDSEKV 1268
Qy 750 QHALDKARTGRTCLVYTHRLSATOADLIVLEHNGKIKSGTHQBELLRNRDIYFKLVNAQ 809
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Db 1329 SL 1330

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Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2004, 01:23:03 ; Search time 877 Seconds

(without alignments)
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Title: US-09-873-409-2

Perfect score: 4079

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUPFIX=xrpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -USER=US09873409 @CGN 1 1 553 @runat_24062004_153028_16726
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA: *
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19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	4079	100.0	2856	9	US-09-873-409-10	Sequence 10, Appl
2	4079	100.0	3177	9	US-09-873-409-12	Sequence 12, Appl
3	4079	100.0	3621	9	US-09-873-409-14	Sequence 14, Appl
4	4079	100.0	3702	9	US-09-873-409-13	Sequence 13, Appl
5	3919	96.1	3699	16	US-10-415-378-34	Sequence 34, Appl
6	3456	84.7	2066	9	US-09-873-409-9	Sequence 9, Appl
7	3168.5	77.7	4091	13	US-10-032-900A-303	Sequence 303, App
8	2465.5	60.4	3825	17	US-10-383-112-48	Sequence 48, Appl
9	2465.5	60.4	3924	9	US-09-880-107-2299	Sequence 2299, Ap
10	2465.5	60.4	3924	17	US-10-641-643-1168	Sequence 1168, Ap
11	2441	59.8	3852	15	US-10-101-433A-1	Sequence 1, Appl
12	2441	59.8	4186	17	US-10-619-359A-1	Sequence 1, Appl
13	2441	59.8	4195	17	US-10-619-359A-3	Sequence 3, Appl
14	2441	59.8	4369	9	US-09-769-037-1	Sequence 1, Appl
15	2441	59.8	4425	9	US-09-769-037-3	Sequence 3, Appl
16	2438	59.8	4317	14	US-10-044-671-1	Sequence 1, Appl
17	2436	59.7	3860	9	US-09-866-866A-1	Sequence 1, Appl
18	2436	59.7	3860	9	US-09-866-866A-3	Sequence 3, Appl
19	2436	59.7	4533	13	US-09-805-020-30	Sequence 30, Appl
20	2436	59.7	4643	14	US-10-072-621-2	Sequence 2, Appl
21	2436	59.7	4643	15	US-10-097-340-1	Sequence 1, Appl
22	2436	59.7	4643	15	US-10-007-926A-258	Sequence 258, App
23	2436	59.7	4646	17	US-10-641-643-1167	Sequence 1167, Ap
24	2436	59.7	4646	17	US-10-343-657-1	Sequence 1, Appl
25	2436	59.7	8630	9	US-09-306-417-2	Sequence 1, Appl
26	2436	59.7	8630	9	US-09-306-417-2	Sequence 2, Appl
27	2431.5	59.6	3912	9	US-09-917-800A-1560	Sequence 1560, Ap
28	2425	59.5	4788	9	US-09-866-866A-7	Sequence 7, Appl
29	2404.5	58.9	4189	9	US-09-866-866A-5	Sequence 5, Appl
30	2372	58.2	4254	9	US-09-917-800A-1424	Sequence 1424, Ap
31	2372	58.2	4254	12	US-10-152-319A-1484	Sequence 1484, Ap
32	2372	58.2	4254	16	US-10-388-934-265	Sequence 265, App
33	2013.5	49.4	5010	9	US-09-917-800A-483	Sequence 483, App
34	1694	41.5	4175	9	US-09-749-340-3	Sequence 3, Appl
35	1694	41.5	4175	15	US-10-456-815-3	Sequence 3, Appl
36	1690.5	41.4	4002	9	US-09-758-828-1	Sequence 1, Appl
37	1690.5	41.4	4002	9	US-09-758-828-3	Sequence 3, Appl
38	1678.5	41.1	3512	9	US-09-749-340-7	Sequence 7, Appl
39	1678.5	41.1	3512	15	US-10-456-815-7	Sequence 7, Appl
40	1669.5	40.9	3861	9	US-09-938-842A-2237	Sequence 2237, Ap
41	1669.5	40.9	3861	11	US-09-938-842A-2237	Sequence 2237, Ap
42	1617	39.6	2698	9	US-09-749-340-5	Sequence 5, Appl
43	1617	39.6	2698	15	US-10-456-815-5	Sequence 5, Appl
44	1606	38.4	3921	16	US-10-280-238-848	Sequence 848, App
45	1586.5	38.9	2905	13	US-10-425-114-34865	Sequence 34865, A

ALIGNMENTS

RESULT 1

US-09-873-409-10
; Sequence 10, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-10

Alignment Scores:	0	Length:	2856
Pred. No.:	4079.00	Matches:	812
Score:			

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9
DB: 9

Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-873-409-2 (1-812) x US-09-873-409-10 (1-2856)

QY 1 MetValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGly 20
DB 418 ATGTGTGATGAGATGACATCAGAGCTTTAAATGTGGGCAATATCGAGACCAATATTGGA 477
QY 21 ValValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGly 40
DB 478 GTGGTTAGTCAGAGCGCTGTTTGTTCGGGACCAACCATCAGTAACATATCAAGTATGGA 537
QY 41 ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
DB 538 CGAGATGATGTGATGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
QY 61 PheIleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMet 80
DB 598 TTTATCATGGAGTTTCTTAATAATTTAATACATGTGTAGGGGAAAAGAGCTCAATG 657
QY 81 SerGlyGlnLysGlnArgIleAlaIleAlaAlaArgAlaLeuValArgAsnProLysIle 100
DB 658 AGTGGAGGCGAAGAGAGAGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 101 LeuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 120
DB 718 CTGATTTTAGATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 121 AlaLeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
DB 778 GCACCTGAGAGAGGCGAGCAAGGTCGGACTACATCTGTTGGTAGCACACCGACTTTCTACT 837
QY 141 IleArgSerAlaAsnLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAla 160
DB 838 ATTCGAAGTGCAGATTTGATTTGACCCCTAAAGATGCAATGCTGCGGAGAGAGAGGACA 897
QY 161 HisAlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle 180
DB 898 CATGCTGAACATAATGGCAAAACGAGGTCATATATTACTTGTGATGTCACAGGATATT 957
QY 181 LysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSer 200
DB 958 AAAAAAGCTGATGAACAGATGAGTCAATGACATATTCTACTGAAGAAAGACCACTCA 1017
QY 201 LeuProLeuHisSerValLysSerIleLysSerAspPheIleAspLysAlaGluGluSer 220
DB 1018 CTTCCTCTGCACTCTGTGAGAGAGATCAAGTCAGACTTCATTGACAGGCTGAGGAATCC 1077
QY 221 ThrGlnSerLysGluIleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsn 240
DB 1078 ACCCAATCTAAAGAGATAAGTCTTCTCAAGTCTCTCTATTAAAAATTTTAAAGTTAAAC 1137
QY 241 LysProGluTyrProPheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
DB 1138 AAGCTTGATGGCTTTTGTGGTCTGGGACATTTGGCTTCTGTCTTAATTTGAATGACTGT 1197
QY 261 HisProValPheSerIleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys 280
DB 1198 CATCCAGTATTTTCCATCATCTTTGCCAAAAATTAACCATGTTTGGAAATTAATGATAAA 1257
QY 281 ThrThrLeuLysHisAsnAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle 300
DB 1258 ACCCATTAAGCATGATGCGAAATTTATTTCCATGATATTCGTTCATTTTGGGTGTTATT 1317
QY 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
DB 1318 TGCCTTGTGCTGATTTTTCATGCGAGGATTTATTTAAGGAGAGAGAGAGAGAGAGAGAG 1377
QY 321 MetArgLeuArgHisLeuAlaPheIysAlaMetLeuTyrGlnAspIleAlaTyrPheAsp 340

DB 1378 ATGAGATTAGACACTTGGCCCTTCAAGCCATGTTATATATCAGGATATTCCCTGCTTGTAT 1437
QY 341 GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
DB 1438 GAAAGCGAAAAACAGACACAGAGGCTTTGACAACAATATTAGCCATATAGCACAAAT 1497
QY 361 GlnGlyAlaThrClySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
DB 1498 CAAGGAGCAACAGGTTCCAGGATGGCGTCTTAACACAAATGCAACTAACATGGGACIT 1557
QY 381 SerValIleIleSerPheIleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAla 400
DB 1558 TCAGTTATCATTTCTTTATATATGATGGAGATGACATTCCTGATTCAGTATTGCT 1617
QY 401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
DB 1618 CCAGTACTTTGCCGTGACAGGAATGATTTGAACCGCAGCAATGACGTGATTTGCCACAAA 1677
QY 421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
DB 1678 GATAACGAGAACTTAAGCATGCTCGAAGATAGCAACTGAAGCTTTGAGAAATATACGT 1737
QY 441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln 460
DB 1738 ACTATAGTGTCTATTAAACAGGAAAAAGCCTTCGAGCAATGTTATGAAGAGATGCTTCAG 1797
QY 461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSer 480
DB 1798 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTTTGGAACTGTTATTCATTCAGC 1857
QY 481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
DB 1858 CATGCTTTATATATTTCCTATATGACAGGAGTTTCGATTTGGAGCCTTAATTAATTCAA 1917
QY 501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla 520
DB 1918 GCTGGACGAAATGACCCAGAGGCGATGTTCTAGTATTTTACGCAATTCATATGAGCT 1977
QY 521 MetAlaIleGlyIleThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
DB 1978 ATGGCCATCGAAAAACGCTCGTTTGTGCTCTGATATATCCAAAGCCAAATTCGGGGCT 2037
QY 541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
DB 2038 GGCATCTGTGTGCTTGTGGAAAGAAACCAATATAGACAGCCGCGAGTCAAGAGGG 2097
QY 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPheTyrPro 580
DB 2098 AAAAGCCAGACACATGTGAAGGAAATTTAGAGTTTCGAGAAGTCTCTTTCTTCTATCCA 2157
QY 581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
DB 2158 TGTGCCCCAGATGTTTCTCTCGTGGCTTATCCCTCAGTATTAGCGAGGAAGACACA 2217
QY 601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
DB 2218 GTAGCAATTTGTGGGAGACAGCGCTGTGGGAAAGACACTTCTGTTCACTTCTGACAGA 2277
QY 621 LeuTyrAspProValGlnGlyValLeuPheAspGlyValAspAlaLysGluLeuAsn 640
DB 2278 CTTTATGACCCCGTGCAGACAGCAAGTGTGTTGATGTGTGGTGTGGATGCAAAAATTTGAT 2337
QY 641 ValGlnTyrLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660
DB 2338 GTACAGTGTCTGCTTCCCAATFAGCAATCTGTTCTCTCAGAGCCTGTGCTCTTCACTGC 2397
QY 661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680
DB 2398 AGCATTTGCTGAAACATCGCTTATGTGACAAACAGCCGCTGTGTGCTTATAGTAGATC 2457
QY 681 LysGluAlaAlaAsnAlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyr 700
DB 2458 AAAGAGCCGCAATGACGCAATATCCATTTCTTTTAAAGGCTCTCCTCAGAAATAC 2517

QY 701 AsnThrGlnValGlyLeuIysGlyAlaGlnLeuSerGlyGlyGlnIysGlnArgIleuAla 720
DB 2518 AACACACAAAGTTGGACTGAAAGGAGCACAGCTTTCTGGGGCCAGAAACAAAGACTAGCT 2577
QY 721 IleAlaArgAlaLeuLeuGlnIysProIysIleLeuLeuLeuAspGluAlaThrSerAla 740
DB 2578 ATGCGAAGGCTCTCTCCAAACCCAAATTTATTTGTTGATGAGGCCACTTCAGCC 2637
QY 741 LeuAspAsnAspSerGluIysValValGlnHisAlaLeuAspLysAlaArgThrGlyArg 760
DB 2638 CTCGATAATGACAGTCAGAAAGGTGGTTTCAGCATGCCCTTGATAAAGCCAGGACGGAGG 2697
QY 761 ThrCysLeuValValThrHisArgIleuSerAlaIleGlnAsnAlaAspLeuIleValVal 780
DB 2698 ACATGCTAGTGTGCTCACTCACAGGCTCTCTGCAATTCAGAACCGAGATTGATAGTGGTT 2757
QY 781 LeuHisAsnGlyIysIleLysGluGlnGlyThrHisGlnGlnLeuLeuArgAsnArgAsp 800
DB 2758 CTCGCAATGTAAGATAAGAAACCAAGCACTCATCAAGAGCTCTCTGAGAAATCGAGAC 2817
QY 801 IleTyrPheIysLeuValAsnAlaGlnSerValGln 812
DB 2818 ATATATTTTAAGTTAGTGAATGCACAGTCAGTGCAG 2853

RESULT 2
US-09-873-409-12
; Sequence 12, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Sayegh, Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 3177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1e
; LOCATION: (198)...(198)
; OTHER INFORMATION: n at position 198 represents any nucleotide (A, T, C or G)
US-09-873-409-12

Alignment Scores:
Pred. No.: 0 Length: 3177
Score: 4079.00 Matches: 812
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-873-409-2 (1-812) x US-09-873-409-12 (1-3177)

QY 1 MetValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGly 20
DB 739 ATGGTGATGAGATGACATCAGAGCTTAAATGTGGCGCATATTCGAGACCATATGGA 798
QY 21 ValValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGly 40
DB 799 GTGGTTAGTCAAGAGCGCTGTTTGTTCGGGACCCACCATCAGTAACAATATCAAGTATGGA 858
QY 41 ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
DB 859 CGAGATGATGTACTGATGAGAGATGGAGAGCGAGCGAGGAGGAGCAATCCGTATGAT 918
QY 61 PheIleMetGluPheProAsnIysPheAsnThrLeuValGlyGluLysAlaGlnMet 80

DB 919 TTTATCATGGAGTTCTCTAATAAATTTAATACATTTGGTAGGGAAAAAGGAGCTCAATG 978
QY 81 SerGlyGlyGlnIysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProIysIle 100
DB 979 AGTGAGGCGCAAGAACAGAGGATCGCAATTTGCTGCTCTAGTTTCGAAACCCCAAGATT 1038
QY 101 IleuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 120
DB 1039 CTGATTTTAGATGAGGCTACGCTCTGCCCTGATTCAGAAAGCAAGTCAGCTGTTTCAAGCT 1098
QY 121 AlaLeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
DB 1099 GCACGTGAGAGCGGAGCAAGAGTGGACTACATCGTGTAGGACACCCGACTTTCTACT 1158
QY 141 IleArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAla 160
DB 1159 ATTCGAGTGCAGATTTTCATTGTCACCTTAAAGGATGGAATGCTGGCGGAGAAAGAGCA 1218
QY 161 HisAlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle 180
DB 1219 CATGCTGAACCTATGCGCAAAACGAGGCTATATTATTACCTTGTGATGTCACAGATATT 1278
QY 181 LysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSer 200
DB 1279 AAAAAAGCTGATGAACAGATGGAGTCAATGACATATTCTACTGAAAGAAAGACCAACTCA 1338
QY 201 LeuProIleuHisSerValLysSerIleLysSerAspPheIleAspLysAlaGluLysSer 220
DB 1339 CTTCCTCGCACTCTGTGAGAGCATCAAGTCAGACTTCATTCAGACGCTGAGGAATCC 1398
QY 221 ThrGlnSerLysGluIleSerLeuProGluValSerLeuLysIleLeuLysLeuAsn 240
DB 1399 ACCCAATCTAAAGAGATAAGTCTCTCTGAGCTCTCTATTAAAAATTTTAAAGTTAAAC 1458
QY 241 LysProGluTyrProPheValValIleGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
DB 1459 AAGCTGTAATGGCTTTTGTGGTCTCGGGACATGGCTTCTGTTCTAAATGGAACTGTT 1518
QY 261 HisProValPheSerIleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys 280
DB 1519 CATCCAGTATTTTCCATCATCTTTGCCAAAAATTTATAACCATGTTTGGAAAAAATATGATAA 1578
QY 281 ThrThrIleuLysHisAspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle 300
DB 1579 ACCACATTTAAAGCATGATGTCAGAAATTTATTCCATGATATTTCGTCATTTTGGGTGTTATT 1638
QY 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
DB 1639 TGCTTTGTCAGTTATTTTCATCGAGGATTTATTTACGCGAGAGCGAGGGAATTTTAACG 1698
QY 321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAsp 340
DB 1699 ATGAGATTAGACACTTGGCTTCAAAGCCATGTTATATCATCAGGATATTGCTGTTGTTGAT 1758
QY 341 GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
DB 1759 GAAAGGAAAAACAGCAGAGGAGGCTTGACAAATATTAGCCATAGATATAGCAAAATT 1818
QY 361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAspMetGlyLeu 380
DB 1819 CAAGGAGCAACAGGTTCCAGGATTTCCAGGATTTGGCTTTAAACAAAAATGCAACTAACATGGAGCTT 1878
QY 381 SerValIleIleSerPheIleTyrGlyTrpGluMetThrPheLeuIleLeuSerIleAla 400
DB 1879 TCGTATATCATTTCTCTTTATATATGAGTGGAGATGACATTCCTTGATTTCTGAGTATTGCT 1938
QY 401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
DB 1939 CCAGTACTTCCGCGGACAGGAATGATTTGAAACCCGACCAATGACTGGATTTTGCACAAACA 1998
QY 421 AspLysGlnLeuLysHisAlaGlyIysIleAlaThrGluAlaLeuGluAsnIleArg 440
DB 1999 GATAAGCAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAAGCTTTGGAGATATACGT 2058

201 LeuProLeuHisSerVallySerIleLeuSerAspPheIleAspLysAlaGluGluSer 220
1783 CTTCCCTCTGCACTCTGTGAAGAGCATCAAGTCAAGTTCATTGACAAAGGCTCAGGAATCC 1842
221 ThrGlnSerLysGluIleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsn 240
1843 ACCCAATCTAAAGAGATAAGTCTTCCTGAAGTCTCTCTATTAATAAATTTTAAAGTTAAAC 1902
241 LysProGluTrpProPheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
1903 AAGCCCTGAATGGCTTTTGTGGTCTTGGGACATGGCTTCTGTCTTAATAATGAACTGTT 1962
261 HisProValPheSerIleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys 280
1963 CATCCAGTATTTCATCATCTTTGCGCAAAATTAACCATGTTTGGAAATATGATAAA 2022
281 ThrThrLeuLysHisAspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle 300
2023 ACCACATTAAGCATGATGACGAAATTTATTCATGATATTCGTCAATTTTGGGTGTATT 2082
301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
2083 TGTCTTCTCAGTTATTTCATGAGGATTTATTTAGCGGACGACGAGGGGAAATTTTACG 2142
321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAsp 340
2143 ATCAGATTAAGACACTTGGCCCTTCAAGGCCATGTTATATCAGGATATTCCTGGATTGAT 2202
341 GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
2203 GAAAGGAAACAGCAGAGGCTTGACMACAATATTATGCCATATAGATATAGACAAAT 2262
361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
2263 CAAGGAGCAACAGGTTCCAGGATTGGCGCTTAACACAAATTCGAATCAACATGGGACTT 2322
381 SerValIleIleSerPheIleTyrGlyTrpGluMetThrPheLeuIleLeuSerIleAla 400
2323 TCAGTTATCATATTCCTTTATATGATGATGGAGATGACATTCCTGATTTCTGAGTATTGCT 2382
401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
2383 CCAGTACTTCCCTGACAGGAATGATTGAACCCGACGACATGATGATTTGCCAACAA 2442
421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
2443 GATAAGCAGACACTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGT 2502
441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln 460
2503 ACTATAGTGTCAATTAACAGGGGAAAAGGCTTCGACCAATGTATGAGAGATGCTTCAG 2562
461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSer 480
2563 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTAATTTGGAAGCTGTTATGCAATTCAG 2622
481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
2623 CATGCCCTTTATATTTTGCCTATGACGAGGGTTTCGATTTGGAGCCCTATTTAATTCAA 2682
501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla 520
2683 GCTGGAGCAATGATCCCGACAGGGCCATGTTTCATAGTTTCTACTGCAATTCATATGGAGCT 2742
521 MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
2743 ATGCCCATCGAAAAACGCTCGTTTGGCTCCTGAATATTCCAAAGCCCAATTCGGGGCT 2802
541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
2803 GCGCATCTGTTGCTTGTGGAAAGAAACCAATATAGACAGCCGAGTCAAGAGGG 2862

561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrPro 580
2863 AAAAAGCCAGACACATGTGAAGGGAATTTAGATTTCCAGAGTCTCTCTTCTTATCCA 2922
581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
2923 TGTCCGCCAGATGTTTTCATCCTCCGTGGCTTATCCCTCAGTATTGAGCGAAGACCA 2982
601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
2983 GTAGCATTTGTGGGAGGACGGCTGTGGGAAAGACATCTCTGTCACTTCTGCAGAGA 3042
621 LeuTyrAspProValGlnGlyValLeuPheAspGlyValAspAlaLysGlnLeuAsn 640
3043 CTTTATGACCCCGTCCAAAGCACAGTGTGTATGTGTGTGGATGCAAAAGATTTGAT 3102
641 ValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660
3103 GTACAGTGGCTCCGTTCCCAATAGCAATGCTTCTCAAGAGCCGTGTCTTCAACTGC 3162
661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680
3163 AGCATTTGCTGAGAACATCGCTATGTGACAAACCCGCTGTGTGTCCTATTAGATC 3222
681 LysGluAlaAlaAsnAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyr 700
3223 AAAGAAAGCCGCAATTCGAGCAAAATATCCATCTTTTATTGAAGGTCTCCCTGAGAAATAC 3282
701 AsnThrGlnValGlyLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAla 720
3283 AACACACAGTTGGACTGAAGGACACAGCTTTCTGGCGGCCGACAAACAAAGACTAGCT 3342
721 IleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAla 740
3343 ATTGCAAGGGCTCTTCTCCAAAACCCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCC 3402
741 LeuAspAsnAspSerGluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArg 760
3403 CTCGATATGACGTGAGAGTGGTTTCAGCATGCCCTTGATTAAGCCAGGACGCGAAGG 3462
761 ThrCysLeuValValThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValVal 780
3463 ACATGCCGTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAAACGACAGATTTGATAGTGGT 3522
781 LeuHisAsnGlyLysIleGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAsp 800
3523 CTGCAATATGGAAGATTAAGAGAACAGAACTCATCAAGAGCTCTCTGAGAAATCGAGAC 3582
801 IleTyrPheLysLeuValAsnAlaGlnSerValGln 812
3583 ATATATTTTAAGTTAGTGAATGACAGTCAGTCAGTCAG 3618

RESULT 4

US-09-873-409-13
; Sequence 13, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 3702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1e
; LOCATION: (723)...(723)

OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)
us-09-873-409-13

Alignment Scores:

Pred. No.: 0 Length: 3702
Score: 4079.00 Matches: 812
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-873-409-2 (1-812) x US-09-873-409-13 (1-3702)

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Qy 1 MetValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGly 20
Db 1264 ATGGTGGATGGAATGACATCAGAGCTTTAAATGTGGCGCATATTCGAGACCATATGGA 1323

Qy 21 ValValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGly 40
Db 1324 GTGGTTAGTCAAGAGCCGTGTTTGTGGGACCACCATCACTAACAATATCAAGTATGGA 1383

Qy 41 ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
Db 1384 CGAGATGATGTGACTGATCAAGAGATGGAGAGCGAGAGGAGCAAGGAAAGCAATGCGTATGAT 1443

Qy 61 PheIleMetGluPheProAsnIysPheAsnThrLeuValGlyGluLysGlyAlaGlnMet 80
Db 1444 TTTATCATGGAGTTTCTTAATAAATTTAATACATTTGGTAGGGGAAAAGGAGCTCAATG 1503

Qy 81 SerGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIle 100
Db 1504 AGTGGAGGCGAGAAACAGAGGATCGCAATGCTGCTGCTTAGTTTCGAAACCCCAAGATT 1563

Qy 101 LeuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 120
Db 1564 CTGATTTTAGATGAGCTACGTCCTGCTGCTGATTCAGAAAGCAGTACGCTGCTTCAAGCT 1623

Qy 121 AlaLeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
Db 1624 GCATCGAGAGCGGAGCAAGGTCGAGCTCAATCGTGGTAGCACACCGGACTTTCTACT 1683

Qy 141 IleArgSerAlaAspIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAla 160
Db 1684 ATTCAAGTGCAGATTGATGTGACCTTAAGGATGGAATGCTGGCGGAAAGGAGCA 1743

Qy 161 HisAlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle 180
Db 1744 CATGCTGAACTAATGGCAAAACGAGGCTATATATTCTCATCTGTGATCTCAGGATATT 1803

Qy 181 LysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSer 200
Db 1804 AAAAAGCTGATGAACAGATGGAGTCAATGACATATTCTACTGAAGAAGAACCAACTCA 1863

Qy 201 LeuProLeuHisSerValLysSerIleLysSerAspPheIleAspLysAlaGluGluSer 220
Db 1864 CTTCCTCTGCATCTGTGAGAGCATCAAGTCAGACTTCATTCAGCAAGGCTGAGGAATCC 1923

Qy 221 ThrGlnSerLysGluIleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsn 240
Db 1924 ACCCAATCTAAAGAGATAAGTCTTCTCGAAGTCTCTATTAATAAATTTTAAAGTTAAAC 1983

Qy 241 LysProGluTyrProPheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
Db 1984 AAGCTCGAATGGCCCTTTGTGTTCTGGGACATTTGGCTTCTCTTAATGGAACTGTT 2043

Qy 261 HisProValPheSerIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys 280
Db 2044 CATCCAGTATTTTCCATCATCTTTGCCAAAATTTATAACCATGTTTGGAAATTAATGATAA 2103

Qy 281 ThrThrLeuLysHisAspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle 300
Db 2104 ACCACATTAAGCATGATGCAGAAATTTATTTCATGATATTCTCATTTTGGGTGTTATT 2163

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Qy 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
Db 2164 TGCTTTGTCTAGTTATTTTCATGCGAGGATTTATTTACGGCAGAGCAGGGGAAATTTTAAACG 2223

Qy 321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAsp 340
Db 2224 ATGAGATTAAAGACACTTGGCTTCAAGGCCATGTTATATACAGGATATTGCTGTTTGAT 2283

Qy 341 GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
Db 2284 GAAAAGGAAAACAGCAGCAGAGGCTTTGACACAAATATTAGCCATAGATATAGCACAAT 2343

Qy 361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
Db 2344 CAAGAGACACAGGTTCCAGGATGGCTTTTAAACCAAAATGCAACTTACATCGGACCT 2403

Qy 381 SerValIleIleSerPheIleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAla 400
Db 2404 TCAGTTATCATTTTCTTTATATATGATGGAGATGACATTCCTGATTTCTGAGTATTGCT 2463

Qy 401 ProValIleAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
Db 2464 CCAGTACTTTCCTGTCAGGATGATTTGAAACCCGAGCAATGACTGGATTTGCCACAAA 2523

Qy 421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
Db 2524 GATAAGCAAGAACTTAAGCATGCTGAAAGATAGCAACTGAAGCTTTGGAGAAATATACGT 2583

Qy 441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln 460
Db 2584 ACTATAGTGTCAATTAACAAAGGAAAGCCCTTCAGCAATATGATGAAGAGATGCTTCAG 2643

Qy 461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSer 480
Db 2644 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTTATGGAAGCTGTATGCAATTCAG 2703

Qy 481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
Db 2704 CATGCCCTTATATATTTTGCCTATGTCAGCAGGGTTTCGATTTTGGAGCCCTAATTTAAATCAA 2763

Qy 501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla 520
Db 2764 GCTGGACGATGATCCCGAGGAGCATGTTCTATAGTTTCTTACTGCAATTCATATGAGCT 2823

Qy 521 MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysLysLysSerGlyAla 540
Db 2824 ATGCCATCGGAAAAACGCTCGTTTGGCTCTCGAAATATTTCCAAAGCCAAATCGGGGCT 2883

Qy 541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
Db 2884 GCGCATCTGTTTGCCTTGTGTAAGAAAGAACCAATATAGACAGCCGAGCTCAAGAAAGG 2943

Qy 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrPro 580
Db 2944 AAAAAGCCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAGCTCTCTTTCTCTATCCA 3003

Qy 581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
Db 3004 TGTGCCCCAGATGTTTTCATCTCCCGGGCTTATCCCTCAGTATTGAGCGGAGGAAGACA 3063

Qy 601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
Db 3064 GTAGCATTTTGGGAGCAGCGCTGTGGGAAAAGCACTTCTGTTCAACTTCTGACAGA 3123

Qy 621 LeuTyrAspProValGlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsn 640
Db 3124 CTTTATGACCCCGTGAAGGACCAAGTCTGTTGATGGTGTGGATGCAAAAGAAATTTGAT 3183

Qy 641 ValGlnTyrLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660
Db 3184 GTACAGTGGCTCGGTTCCCAATAGCAATCGTTCTCAAGAGCTGTGCTCTTCAACTGC 3243

Qy 661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680

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Qy 281 ThrThrLeuLysHisAspAlaGluLeuTyrSerMetIlePheValIleLeuGlyValIle 300
Db 2179 ACCACATTTAAAGCATGATGACAGAAATTTATTCATGATATTCGTCAATTTGGGTGTTATT 2238
Qy 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
Db 2239 TGCCTTGTCACTTAATTCATG----- 2259
Qy 321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAsp 340
Db 2260 -----CAGGATATTGCGTGGTTGAT 2280
Qy 341 GlnLysGlnAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
Db 2281 GAAAGGAAACACACACAGGAGGCTTGACACAAATATTAGCCATAGATATAGCACAAATT 2340
Qy 361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
Db 2341 CAAGGAGCAACAGGCTCCAGGATTTGGCTTTAACACAAATGCACTTAACATGGGACTT 2400
Qy 381 SerValIleIleSerPheIleTyrGlyTyrGluMetThrPheIleIleLeuSerIleAla 400
Db 2401 TCAGTTATCATTTCTCTTATATATGAGTGGAGATGATCATTCCTGATTTCTGAGTATTGCT 2460
Qy 401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
Db 2461 CCAGTACTTGGCTGACAGGATGATTTGAACCCGACGATGACTGGATTTGCCACAAA 2520
Qy 421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
Db 2521 GATAAGCAAGAACTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGT 2580
Qy 441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln 460
Db 2581 ACTATAGTGTCTTTAAACAGGGAAGAAAGCCCTTCAGCAATGATGATGAAGATGCTTCAG 2640
Qy 461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSer 480
Db 2641 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTTATGGAAGCTGTTATGCAATTCAGC 2700
Qy 481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
Db 2701 CATGCCCTTATATTTTGGCTATGCGCGAGGTTTCGATTTGGAGCTTATTAATTCAA 2760
Qy 501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla 520
Db 2761 GCTGGAGCAATGACCCAGAGGGCATGTTTCATAGTTTTTACTGCAATTTGCATATGGAGCT 2820
Qy 521 MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
Db 2821 ATGCCCATCGAGAAACGCTCGTFTTGGCTCCTCGATATTTCCAAAGCCAAATCGGGGCT 2880
Qy 541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
Db 2881 GCGCATCTGTTTGTCTTGTGGAAAGAAACCAATATACACAGCCGCACTCAAGAAGGG 2940
Qy 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrPro 580
Db 2941 AAAAAGCCAGACACATGTGAAGGAAATTTAGATTTTCGAAAGTCTCTTTCTTCATCCA 3000
Qy 581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
Db 3001 TGTGCCCCAGATGTTTTCATCTCTCGTGGCTTATCTCTCATGATTTGCGCAGCAAGACA 3060
Qy 601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
Db 3061 GTAGCATTTGTGGGGAGCAGCGGCTGTGGGAAAGCACTTCTGTTCAACTTCTGCAAGAGA 3120
Qy 621 LeuTyrAspProValGlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsn 640
Db 3121 CTTTATGACCCCGTGCAGGACAGTGTCTTTGATGTGTGGATGCAAAAGAAATTCAT 3180
Qy 641 ValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660

Db 3181 GTACAGTGGCTCGTTCCTCCAAATAGCAATCGTTCTCTCAAGAGCCTGTGCTCTTCAACTGC 3240
Qy 661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680
Db 3241 AGCATTTGCTGAGAACATCGCTATGTGACACAGCCGTGTGTGCCATTAGATGAGATC 3300
Qy 681 LysGluAlaAlaAsnAlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyr 700
Db 3301 AAAGAAGCCGCAATCGACAAATATCCATTTCTTTTATTGAAAGTCTCCCTCGAGAAATAC 3360
Qy 701 AsnThrGlnValGlyLeuLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAla 720
Db 3361 AACACAAAGTTGGAGCTGAAGAGGACACAGCTTTCTGGCGGCCAGAAACAAAGACTAGCT 3420
Qy 721 IleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAla 740
Db 3421 ATTGCAAGGCTCTTCTCTCAAAACCCAAAATTTTATTGTTGATGAGGCCACTTCAGCC 3480
Qy 741 LeuAspAsnAspSerSerCysLysValValGlnHisAlaLeuAspLysIleArgThrGlyArg 760
Db 3481 CTCGATAATGACAGTGAAGGTGGTTTCAGCATGCCCTTGTATAAGCCAGGAGGGAAGG 3540
Qy 761 ThrCysLeuValValThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValVal 780
Db 3541 ACATGCTTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAACGAGATTTGATAGTGT 3600
Qy 781 LeuHisAsnGlyLysIleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAsp 800
Db 3601 CTGCAAAATGGAAGATAAAGCAAGAACTCATCAAGAGCTCTCTGAGAAATCGAGAC 3660
Qy 801 IleTyrPheLysLeuValAsnAlaGlnSerValGln 812
Db 3661 ATATATTTAAAGTTAGTGAATCCACAGTCAGTGCAG 3696

RESULT 6

US-09-873-409-9
; Sequence 9, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-9

Alignment Scores:
Pred. No.: 0 Length: 2066
Score: 3456.00 Matches: 687
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.73% Indels: 0
DB: 9 Gaps: 0

US-09-873-409-2 (1-812) x US-09-873-409-9 (1-2066)

Qy 126 SerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIleArgSerAlaAsp 145
Db 3 ACCAAAGGTGCGAGCTACAAATCGTGTGTAGCACACACCGACCTTCTTACTATTTCGAAGTGCAGAT 62
Qy 146 LeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyValHisAlaGluLeuMet 165
Db 63 TTGATTGTGACCTTAAAGGATGGAATGCTGGCGGAGAAAGGAGACATGCTGTAACATAATG 122

166 QY AlalysArgGlyLeuTyrThrSerLeuValMetSerGlnAspIleLysLysAlaAspGlu 185
123 DB GCAAAACAGGCTCTATATTACTTGTGATGTCACAGGATATTAATAAAGCTGATGA 182
186 QY GlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSerLeuProLeuHisSer 205
183 DB CAGATGGAGTCAATGACATATTTCTACTGAAAGAAAGACCACTCTCTCTGCACTCT 242
206 QY ValLysSerIleLysSerAspPheIleAspLysAlaGluSerThrGlnSerLysGlu 225
243 DB GTGAAGAGCATCAAGTCAGACTTCATTGACAGGCTCAGGAATCCACCCCAATTAAGAG 302
226 QY IleSerLeuProGluValSerLeuLeuLysIleLeuLysIleLeuLysProGluTrrPro 245
303 DB ATAAGTCTCTCTGAGGCTCTCTCTATTAAATAATTTAAAGTTAAACAAGCCCTGAATGCCT 362
246 QY PheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSer 265
363 DB TTGTGTGTTCTGGGGACATTTGGCTCTCTCTTAATTTGGAATGTTCTATCAGTATTTTC 422
266 QY IleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHis 285
423 DB ATCATCTTTGCAAAATTAATAACCATCTTTGGAAATTAATGATAAACCACATTAAGCAT 482
286 QY AsnAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr 305
483 DB GATCGAGAAATTTATTCATGATATTCGTCAATTTGGTGTTATTTCTTTGTCAGTTAT 542
306 QY PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis 325
543 DB TTCATGCGGGATTTATTTACGGCAGACAGCGGGAATTTTAACGATGAGATTAAAGACAC 602
326 QY LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrrPheAspGluLysGluAsnSer 345
603 DB TTGSCCTTCAAGCCATGTTATATTCAGGATATTCCTGTTGATGAAAGGAAACAGC 662
346 QY ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
663 DB ACAGAGGCTTGACACAAATATTAGCCATAGATATAGCACAATTTCAAGGACACACAGT 722
366 QY SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385
723 DB TCCAGGATGCGCTTTAAACCAAAATGCAACTAACATGGGACTTTTCAGTTATCATTTCC 782
386 QY PheIleTyrGlyTrrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
783 DB TTTATATATGATGGGAGATGACATTCCTGATTTCTGATTTCTGAGTATTTCTCAGTACTTCCGCTG 842
406 QY ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
843 DB ACAGGAATGATTGAACCGCAGCAATGACTGATTTGCCAACAAAGATAAGCAAGAACTT 902
426 QY LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445
903 DB AAGCATGCTGGAAAGATAGCAACTGAAGCTTTGAGAAATATACGTACTATAGTGTCAATTA 962
446 QY ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465
963 DB ACAAGGAAAGAGCTTCGAGCAATGATGATGAGAGATGCTTCAGACTCAACACAGAAAT 1022
466 QY ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr 485
1023 DB ACCTCGAAGAAAGCACAGATTTATTGGAAGCTGTTATGCACTTCAGCCATGCTTTATATAT 1082
486 QY PheAlaTrrAlaAlaGlyPheArgPheGlyValatrrLeuIleGlnAlaGlyArgMetThr 505
1083 DB TTTGCCCTATGACGAGGGTTTCGATTTGGAGCTTATTTAATTCAGCTGGACGATGACC 1142
506 QY ProGluGlyMetPheIleValPheThrAlaIleAlaTrrGlyAlaMetAlaIleGlyLys 525
1143 DB CCAGAGGCGCATGTTCAATAGTTTACTGCAATTCATATGAGCTATGGCATCGGAAAA 1202
526 QY ThrLeuValLeuAlaProGluTrrSerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545

1203 DB ACCTCGTCTTTGGCTCTCTGAAATATTCCAAAGCAAAATCGGGGCTCGGCATCTGTTTGCC 1262
546 QY LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565
1263 DB TTGTTGGAAAGAAACCAATATAGACGCCGAGTCAAGAAAGGAAAAAGCCAGACACA 1322
566 QY CysGluGlyAsnLeuGluPheArgGluValSerPheTyrProCysArgProAspVal 585
1323 DB TGTGAAGGAAATTTAGAGTTTCGAGAAGTCTCTTCTCTTATCCATGTGCGCCAGATGTT 1382
586 QY PheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGly 605
1383 DB TTCATCTCTCGTGGCTTATCCCTCAGTATTGAGCGAGAAAGACAGTATTCATTTGGGG 1442
606 QY SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProVal 625
1443 DB ACAGCGGCTGTGGGAAAGACATCTCTGTTCAACTTCTCAGAGACTTTATGACCCCGTG 1502
626 QY GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrrLeuArg 645
1503 DB CAAGGACAAAGTCTGTTTGTATGTTGGATGCAAAAGAAATGGAATGACAGTGGCTCCGT 1562
646 QY SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
1563 DB TCCCAATAGCAATCGTCTCTCAGAGCCTGTGCTCTTCACTGACAGCATTCGTGAGAAC 1622
666 QY IleAlaTrrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsn 685
1623 DB ATGCTTATGTGACAAACAGCGCTGTGTGTCCTCCTAGATGACATCAAGAAAGCCGCAAT 1682
686 QY AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
1683 DB GCAGCAATATCCATCTCTTTTATGAGGTCTCCCTGAGAAATACAAACACAAAGTTGGA 1742
706 QY LeuLysGlyValAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaIleu 725
1743 DB CTGAAAGGAGCAGCATCTTCTGCGGCCAGAAACAAAGACTAGCTATTCAAGGGCTCTT 1802
726 QY LeuGlnLysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
1803 DB CTCCAAAACCCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCCGATATGACAGT 1862
746 QY GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
1863 DB GAGAAGTGGTTTCAGCATGCCCTTGATAAGCCAGGACCGGAAGGACATGCTTAGTGGTC 1922
766 QY ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
1923 DB ACTCAGAGCTCTCTCAATTCAGAACGCGAGATTTGATAGTGTCTTCGACCAATGGAAG 1982
786 QY IleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTrrPheLysLeu 805
1983 DB ATAAAGCAACAGGAATCTCATCAGAGCTCTCTGAGAAATCGAGACATATATTTAAGTTA 2042
806 QY ValAsnAlaGlnSerValGln 812
2043 DB GTGAATGCACAGTCAGTGCAG 2063

RESULT 7

US-10-092-900A-303
; Sequence 303, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muraidhara
; APPLICANT: Spytex, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen

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/ APPLICANT: Gorman, Linda
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Gangolli, Esba A.
/ APPLICANT: Vernet, Corine A.M.
/ APPLICANT: Guo, Xiaojia Sasha T.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Fernandes, Elma R.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Liu Yi
/ APPLICANT: Anderson, David W.
/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Catterton, Elina
/ APPLICANT: Leite, Mario W.
/ APPLICANT: Zhong, Kaihong
/ APPLICANT: Alsobrook, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: No. US20040043382A1 Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-290C
/ CURRENT APPLICATION NUMBER: US/10/092,900A
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: USSN 60/274,322
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: USSN 60/283,675
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: USSN 60/338,092
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/274,281
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: USSN 60/274,191
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: USSN 60/325,681
/ PRIOR FILING DATE: 2001-09-27
/ PRIOR APPLICATION NUMBER: USSN 60/304,354
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: USSN 60/279,995
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: USSN 60/294,899
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: USSN 60/287,424
/ PRIOR FILING DATE: 2001-04-30
/ Remaining prior application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 768
/ SEQ ID NO 303
/ LENGTH: 4091
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (16)..(4078)
/ US-10-092-900A-303

Alignment Scores:
Pred. No.: 7,72e-305 Length: 4091
Score: 3168.50 Matches: 677
Percent Similarity: 80.16% Conservative: 30
Best Local Similarity: 76.76% Mismatches: 62
Query Match: 17.68% Indels: 113
DB: 13 Gaps: 14

US-09-873-409-2 (1-812) x US-10-092-900A-303 (1-4091)

Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Ddb 1378 GTGGAGTGGTGGATGCAAAAGAAATTAAGATGATACAGTGGCTCGTCCCAAAATAGCAATC 1437
Qy 22 ValSerGinGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41

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QY 338 TrpPheAspGluLysGluSerThrGlyLeuThrThrIleLeuAlaIleAspIle 357
DB 2461 TGGTTTGTATGAAAGGAAACACACAGAGGCTTGACAAATATATTAGCCATGATATA 2520
QY 358 AlaGlnIleGlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsn 377
DB 2521 GCACAAATTCAGAGGACACAGGTTCCAGGATTGGGGCTTTAACACACAAATGCACTAAC 2580
QY 378 MetGlyLeuSerValIleIleSerPheIleTyrGlyTyrGluMetThrPheLeuIleLeu 397
DB 2581 ATGGGACTTTCAGTTATATCTTCTTATATATGGATGGAGATGACATTCCTGATCTG 2640
QY 398 SerIleAlaProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPhe 417
DB 2641 AGTATTGCTCCAGTACTTGGCGTGACAGGAATGANTGAAACCGACCAATGACTGGATT 2700
QY 418 AlaAsnIysAspLysGlnGluLeuLysHisAlaGly-----LysIleAlaThrGluAla 435
DB 2701 GCCAAACAAAGATAGCAAGAACTTAAGCATGCTGGAAAGGTAAGATAGCAACTGAAGCT 2760
QY 436 LeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyr 455
DB 2761 TTGGAGATATAGCTACTATAGTGTCTATTAAACAGGAGAAAGCCCTTCAGGACCAATGTAT 2820
QY 456 GluGluMetLeuGlnThrGlnHis----ArgAsnThrSerLysLysAlaGlnIleIleGly 474
DB 2821 GAAGAGATGCTTCAGACTCAACACAGAGAGAAATACCTCGAAGAAAGACAGATTAATGGA 2880
QY 475 SerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPhe 494
DB 2881 AGCTGTTATGCAATGACCATGCTTATATATTTCCTATGCGCAGGGTTTCGATTT 2940
QY 495 GlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPhe---IleValPhe 513
DB 2941 GGAGGCTTATTAAATTCAGCTGACGAATGTCAATGCTTATCTTTTCATAGAGTTTTT 3000
QY 514 ThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValIleAlaProGluTyr 533
DB 3001 ACTGCAATTCATATGAGCTATGGCCATCGGAGAAACGCTGTTTGGCTCTCTGAATAT 3060
QY 534 SerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuGluLysLysProAsnIle 553
DB 3061 TCCAAAGCCAAATCGGGGCTGGCATCTGTTTGCCTTGTGGAAAGAAACCAATATA 3120
QY 554 AspSerArgSerGlnGluGlyLysLysPro-----AspThrCysGluGlyAsnLeu 570
DB 3121 GACAGCGCAGTCAAGAGGAGAAAGCCACTTTTCACAGACACATGTGAAGGAAATTA 3180
QY 571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly 590
DB 3181 GAGTTTCGAGAGCTCTCTTCTTCTATCCATGTGCGCCAGATGTTTCACTCTCCGTGCG 3240
QY 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly 610
DB 3241 TTATCCCTCAGTATTGAGCGAGAAAGACAGTAGCATTTTGGGGAGCAGCGCTGTGGG 3300
QY 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
DB 3301 AAAAGCACCTTCGTTCAACTTCTGCGAGACTTTATGACCCCGTGCAGGACAAACAGCTG 3360
QY 631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArgSerGlnIleAlaIle 650
DB 3361 TTGTATGGTGTGATGATCAAAAGAAATGATGATGACAGTGGCTCGTCTCCCAATAGCAATC 3420
QY 651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp 670
DB 3421 GTTCCTCAAGAGCGCTGCTCTCTTCAACTGACGATTCGCTGAGAACATCCCTATGCTGAC 3480
QY 671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis 690
DB 3481 AACAGCGCTGTGGTGCATTAGTAGATCAAGAGAGCGGCAATGCGCAATATTCAT 3540

QY 691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln 710
DB 3541 TCTTTTATTGAAGTCTCCCT---AAATACACACACAAAGTTGGACTGAAAGAGCACAG 3597
QY 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
DB 3598 CTTTCTGGCGGCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCTCCAAAACCCAAA 3657
QY 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys-----Val 748
DB 3658 ATTATTATTGTTGGATGAGCCACTTCAGCCCTTCGATAATGACAGTGAGAGGTACAGGTG 3717
QY 749 ValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArg 768
DB 3718 GTTCAGCATGCCCTGTTAATAAGCCAGGAGGAGGACATGCTAGTGTCTACTCACAGG 3777
QY 769 LeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGlu 788
DB 3778 CTCTCTGCAATTCAGACCGCAGATTGTAGTGGTCTTCGCAATGGAAAGATAAGGAA 3837
QY 789 GlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAla 808
DB 3838 CAAGGAACTCATCAGAGCTCTCTGGAATCGAGACATATATTTTAAGTTAGTGAATGCA 3897
QY 809 GlnSer 810
DB 3898 CAGTCA 3903

RESULT 8
US-10-363-112-48
; Sequence 48, Application US/10363112
; Publication No. US20040091964A1
; GENERAL INFORMATION:
; APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY
; APPLICANT: HARRIS, PHILLIP
; APPLICANT: HARRIS, MATTHEW
; TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
; FILE REFERENCE: 007643-0302189
; CURRENT APPLICATION NUMBER: US/10/363,112
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/AU01/01093
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,663
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48
; LENGTH: 3825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3825)
; US-10-363-112-48

Alignment Scores:
Pred. No.: 7,65e-235 Length: 3825
Score: 2465.50 Matches: 478
Percent Similarity: 76.46% Conservative: 149
Best Local Similarity: 58.29% Mismatches: 182
Query Match: 60.44% Indels: 11
DB: 17 Gaps: 3

US-09-873-409-2 (1-812) x US-10-363-112-48 (1-3825)

QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1363 ATTGATGGCGAGGATATTAGGAACCTTTTAATGTAACCTATCTGAGGGAATCATTTGGTGG 1422
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1423 GTGAGTCAGGAGCGGTGCTGTTTTCACCAACATGCTGGAATATTTTGTGTGGCGCT 1482

Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAlaAsnAlaTyrAspPhe 61
Db 1493 GGAAATGTACCATGTGATGATTAAGAAAGCTGTCAAGAGGCGCAACGCCCTATGAGTTT 1542
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1543 ATCATGAATATTACACAGAAATTTGACACCTCTGGTTGGAGAGAGAGGGGCCACGCTGAGT 1602
Qy 82 GlyGlyGlnLysGlnArgGluAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 101
Db 1603 GGTGGGCAAGACAGAGGATGCCATTCACGTGCTCCCTGGTTGCAACCCCAAGATCTT 1662
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGlnSerLysSerAlaValGlnAlaAla 121
Db 1663 CTGCTGGATGAGGCCACGCTCAGCATTTGGACACAGAAAGTGAAGCTGAGGTACAGCCAGCT 1722
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValAlaAlaHisArgLeuSerThrIle 141
Db 1723 CTGGAATAAGGCCAGAGAGGGCGGACCACTTGTATGATGATGATGATGATGATGATGATG 1782
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1783 CGAAATGCAGATGTCATCGCTGGGTTTGAGGATGGAGTAATTTGTGGAGCAAGGAGCCAC 1842
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal 175
Db 1843 AGCGAACTGATGAAGAGGAAGGGGTGACTTCAAACTTGTCAACATGTCAGACATCAGGA 1902
Qy 176 -----MetSerGlnAspIleLysLysAlaAspGluGlnMetGluSerMetTyr 192
Db 1903 AGCCAGATCCAGTCAGAGAAATTTGAATAATGATGAAGAGGCTGCCACTAGATGGCC 1962
Qy 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
Db 1963 CCAATAGCTGGAATCTCGCTATTATAGGCATTTCTACTCAGAAAACCTTTAAAAATTC 2022
Qy 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluIleSerLeuProGlu 230
Db 2023 CAATGTGTCAAGAGGCTTGATGTGGAACCGATGACTTGAAGCAATATGTGCCACCA 2082
Qy 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValValLeuGly 250
Db 2083 GTGCTCTTCTGAGGCTCTGAAACTGAATAAAACAGAAATGGCCCTACTTTTGTGCTGGA 2142
Qy 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
Db 2143 ACAGTATGTGCTGCAATGCGGGGCTTCAGCCGGCATTTTCAGTCATATTTCTCAGAG 2202
Qy 271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr 290
Db 2203 ATCATAGCGATTTTGGACCGGCGATGATGTCAGTGAAGCAGCAGAGAGTGCACATATTC 2262
Qy 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
Db 2263 TCTTTGATTTTCTTATTTCTGGATATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCT 2322
Qy 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
Db 2323 AGCTTTGGGAAGCTGGCGAGATCTCTACAGAGAGCTGCGGTCAATGGCTTTTAAAGCA 2382
Qy 331 MetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGlyGlyLeuThr 350
Db 2383 ATGCTAAGACAGAGCATGAGTGGTTTGTATGACCAATAAAACAGACTGCTGCTGCTTCT 2442
Qy 351 ThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArgIleGlyVal 370
Db 2443 ACHAGACTGCCACAGATGCTGCCAGTCCAGAGGAGCCACAGGACCGAGTGGCTTTA 2502
Qy 371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleTyrGlyTrp 390
Db 2503 ATTCAGCAGAAATATAGCTAACCTTGCACTGGTATTATCATATCATATCATATCATATG 2562
Qy 391 GluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGlyMetIleGlu 410

Db 2563 CAGTTAAACCTATTGCTATTAGCAGTTGTTCCAATTATTGCTGTGTCAGGAATTTGTGAA 2622
Qy 411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnLeuLysHisAlaGlyLys 430
Db 2623 ATGAAATTTGTTGGCTGGAAATGCCAAAGAGATATAAAAGAACTGGAGAGCTGCTGGAAAG 2682
Qy 431 IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla 450
Db 2683 ATTGCAACAGAGGCAATAGAAATATTAGCAGAGTTGTCTTTTGACCCAGGAAGAAAA 2742
Qy 451 PheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla 470
Db 2743 TTTGAATCAATGTATGTTGAAAATTTGATGGACCTTACAGGAATTTCTGTGCAAGAGGCA 2802
Qy 471 GlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAla 490
Db 2803 CACATCTATGGAATTACTTTAGTATCTCACAAGCATTTATGATATTTTCCATATGCGGT 2862
Qy 491 GlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPhe 510
Db 2863 TGTGTTTGGATTTGGTGCATATCTCATTTGTAATGGAATGCAATGCGCTTCAGAGATGTTATT 2922
Qy 511 IleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValLeuAla 530
Db 2923 CTGGTGTCTTCTCAATTTGTTGTCAGTGGCTCTAGGACATGCCAGTTCAATTGCT 2982
Qy 531 ProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuLysLys 550
Db 2983 CCAGACTATGCTAAAGCTAAGCTGTCTGCAGCCCACTTATTCTATGCTGTTTGAAGACAA 3042
Qy 551 ProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGluGlyAsnLeu 570
Db 3043 CCTCTGATTGACAGCTACAGTGAAGAGGGGCTGAGCCCTGATAAATTTGAAGAAATATA 3102
Qy 571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly 590
Db 3103 ACATTAAATGAAGTCGTGTTCAACTATCCCAACCCGAGCAACGCTGCAGTGTTCAGGG 3162
Qy 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly 610
Db 3163 CTGAGCTGAGAGTGAAGAAAGCCAGACACTAGCCCTGTGGTGGCAGCAGTGGCTGTGGG 3222
Qy 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
Db 3223 AAGAGCAGCTGTCTCAGCTCTCTGAGCGGTTCTACGACCCCTTGGCGGCGACAGTGTCT 3282
Qy 631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGlnIleAlaIle 650
Db 3283 CTCGATGCTCAAGAACCAAGAACTCAATGTCCAGTGGCTCAGAGCTCAACTCGGAATC 3342
Qy 651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp 670
Db 3343 GTGTCTCAGAGGCTATCTCTTTTGTCTGACAGATTCGCGAGATATTCGCTATGAGAC 3402
Qy 671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis 690
Db 3403 AACAGCCGGTTGTATCAGAGGATGAAATTTGTGAGTGCAGCCAAAGCTGCCAATACAT 3462
Qy 691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyValGln 710
Db 3463 CCTTTTCATCAGAGCTTACCCCAATATGAAACAGAGTGGCAGATTAAGGGAGCTCAG 3522
Qy 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
Db 3523 CTCTCAGGAGGCTCAAAAACAGAGGATTTGTTTGGCCGAGCCCTCATCAGCAACCTCAA 3582
Qy 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLysValValGln 750
Db 3583 ATCTCTCTGTGTGATGAGCTACATCAGCTCTGTGATCTACTGAAAGTGAAGAGTTGTCCAA 3642
Qy 751 HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer 770

Db 3643 GAAGCCCTGGACAAAGCCAGAGAGCGCCACCTGCTATTTGTTGCTCCACCGCTGTCC 3702
Qy 771 AlAtleGlnAsnAlaAspLeuValValLeuHleAsnGlyLysIleGlyVal 790
Db 3703 ACATCCGAAATGAGACTTAATAGTGTGTTTCAGAAATGGAGAGTCAAGAGCATGCGC 3762
Qy 791 ThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
Db 3763 ACAGCATCAGCAGCTGCTGGCACAGAAAGCATCTATTTTCAATGGTCTAGTGTCCAGGCT 3822

RESULT 9

US-09-880-107-2299
; Sequence 2299, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2299
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M23234
US-09-880-107-2299

Alignment Scores:
Pred. No.: 7 95e-235 Length: 3924
Score: 2465.50 Matches: 478
Percent Similarity: 76.46% Conservative: 149
Best Local Similarity: 58.29% Mismatches: 182
Query Match: 60.44% Indels: 11
DB: 9 Gaps: 3

US-09-873-409-2 (1-812) X US-09-880-107-2299 (1-3924)

Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1395 ATTGATGGCGCAGGATATTAGGAACCTTTAATGTAAACTATCTGAGGGAATCATTTGGTGTG 1454
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1455 GTGAGTCGAGGCGCGTGTCTTTCACCACTATGCTGAAATATTGTTATGGCGT 1514
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1515 GGAATGTACCATGGATGAGATAAGAAAGCTGTCAAGAGGCCAACGGCTATGAGTTT 1574
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGlyLysGlyAlaGlnMetSer 81
Db 1575 ATCATGAATTTACCACAGAAATTTGACCCCTGTGTGGAGAGAGGGCCGAGTGTAGT 1634
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1635 GGTGGCAGAGCAGAGATCGCATTTGCAAGTGGCTGCTGCAACCCCAAGATCCTT 1694
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGlnSerLysSerAlaValGlnAlaAla 121
Db 1695 CTGTGATGAGGCGCAGCTCAGCATTTGACACAGAAAGTGAAGTGTGAGGAGGAGCT 1754
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141

Db 1755 CTGGATAAGGCCAGAGAGCGCGACCAATGTGTATAGCACACCGACTGTCTACGGTC 1814
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1815 CGAATGCGAGATGTCATCGCTGGTTTGAGGATGAGTAATTTGTGAGCAAGGAAGCCAC 1874
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal----- 175
Db 1875 AGCGAACTGATCAAGAGAGGAGGGGTACTTCAAACTTGTCAACATGTCAGACATCAGGA 1934
Qy 176 -----MetSerGlnAspIleLysLysAlaAspGluGlnMetGluSerMetThrTyr 192
Db 1935 AGCGAGATCCAGTCAGAGAAATTTGAATTAATGATGAAGAGCTGCCACTAGATGGCC 1994
Qy 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
Db 1995 CCAATGGCTGCAATTCGCTATTTAGGCATTTCTACTCAGAAAAACCTTAAAAATTTCA 2054
Qy 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluLysSerLeuProGlu 230
Db 2055 CAAATGTGTCAAGAGAGCTTGTATGTGAAACCGATGGACTTGAAGCAATGTGCCACCA 2114
Qy 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValValLeuGly 250
Db 2115 GTGTCTTCTCGAAGCTCTGAACTGAATAAAACAGATGCGCTTCTTGTGTGGGA 2174
Qy 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
Db 2175 ACAGTATGTGCCAATTCGCGGGCTTTCAGCGGCAATTTTCAGTCTATTTCTCAGAG 2234
Qy 271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr 290
Db 2235 ATCATAGCGATTTTGGACCGCATGATGATGAGTGAACGACGACGAGTGCACATATTC 2294
Qy 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
Db 2295 TCTTTGATTTTCTTATTTCTGGGAATTTCTTTTCTTTTCTTCTTCTTCTTCTTCTTCT 2354
Qy 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
Db 2355 AGTTTGGAAAGCTGCGAGATCTCCACAGAGACTGCGTCAATGCTTTTAAAGCA 2414
Qy 331 MetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGlyGlyLeuThr 350
Db 2415 ATGTAAAGACAGGACATGAGTGTGTTGATGACCATAAACAGTACTGCTGCACTTCT 2474
Qy 351 ThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArgIleGlyVal 370
Db 2475 ACAAGCTTGGCACAGATGCTCCCAAGTCCCAAGGAGCCACAGAACCCAGGTTGCTTTA 2534
Qy 371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleTyrGlyTyr 390
Db 2535 ATGTCACAGAAATATAGCTTACCTTGGAACTGGTATTTATCATATTTATCTACGGTGG 2594
Qy 391 GluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGlyMetIleGlu 410
Db 2595 CAGTTAAACCTTATGCTATTAGCAGTTGTTCCAAATTTATGCTGTGTCAGGAATTTGTGAA 2654
Qy 411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHisAlaGlyLys 430
Db 2655 ATGAAATTTGCTGGTGGAAATGCCAAAGAGATATAAAGAACTGGAAGCTGCTGGAAG 2714
Qy 431 IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla 450
Db 2715 ATTGCAACAGAGGCAATAGAAAATATTAGGACAGTTGTCTTTGACCCAGGAAGAAAA 2774
Qy 451 PheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla 470
Db 2775 TTGGAATCAATGATGTGTAATAATTTGATGGACCTTACAGAAATTTCTGTCAGAGGCA 2834
Qy 471 GlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAla 490
Db 2835 CACATCTATGGAATTACTTTTAGTATCTCACAAGCATTTATGTAATTTTCTTATGCCGCT 2894

Db 1695 CTGCTGGATGAGCCAGCTCAGCATTTGGACACAGAAAGTGAAGCTGAGGTACAGGCAGCT 1754
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValAlaAlaHisArgLeuSerThrIle 141
Db 1755 CTGGATAAGCCAGAGAGCCGCGACCACTTGTGATAGACACAGCAGCTGTCTACGGTC 1814
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1815 CGAAATGCGATGTCATCGCTGGTGTGGATGGAGTGAATTTGGAGCAAGAGGCCAC 1874
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal----- 175
Db 1875 AGCGAACTGATGAAGAGGAGGGGTGACTTCAAACTTGTCAACATGCAGACATCAGGA 1934
Qy 176 -----MetSerGlnAspIleLysLysAlaAspGluGlnMetGluSerMetThrTyr 192
Db 1935 AGCCAGATCCAGTCAGAGAAATTTGAATAAATGATCAAAAGCTGCCCATAGAAATGGCC 1994
Qy 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
Db 1995 CCAATGGCTGGAAATCTCGCTATTATTAGGCATTCTACTCAGAAACCTTTAAAAATTC 2054
Qy 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluLysSerLeuProGlu 230
Db 2055 CAAATGTGTGAGAGAGCTGTGATGGAAACCGATGGACTTGAAGCAAAATGTGCCACCA 2114
Qy 231 ValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValValLeuGly 250
Db 2115 GTCTCTTCTGAAAGTCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 2174
Qy 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
Db 2175 ACAGTATGTCCTATCCATGGGGGCTTCAGCCGGCATTTTCAGTCATATCTCAGAG 2234
Qy 271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluLysTyr 290
Db 2235 ATCATAGCGATTTTGGACAGCGCATGATGCGATGAGCAGAGAGTGCACCAATATTC 2294
Qy 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
Db 2295 TCTTGTATTTCTTATCTCGGATTAATTTCTTTTACTTTCTCTCTCTCTCTCTCTCT 2354
Qy 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
Db 2355 ACCTTTGGGAAAGCTGCGAGATCTCTCAFCAGAGAGACTCGGTCATATGGCTTTTAAAGCA 2414
Qy 331 MetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGlyGlyLeuThr 350
Db 2415 ATGCTAAGACAGGACATGAGCTGGTTGATGACCATATAAACAGTACTGCTGCACTTTCT 2474
Qy 351 ThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyValThrGlySerArgIleGlyVal 370
Db 2475 ACAAGACTTGGCAGATGCTGCCAAGTCCCAAGGAGCCACAGAGACCAAGTTGGCTTTA 2534
Qy 371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleTyrGlyTyr 390
Db 2535 ATTGCAACAGAAATAGCACTAACCTTGGAACTGGTATTATCATATCATATTTATCTACG 2594
Qy 391 GluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGlyMetIleGlu 410
Db 2595 CAGTTAACTTATGCTATTAGCAGTTGTTCCAAATTTGCTGTGTCAGGAATTTGTTGA 2654
Qy 411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHisAlaGlyLys 430
Db 2655 ATGAAATTTGTGCTGGAAATGCCAAAGAGAGATAAAAGAACTGGAAGCTGCTGGAAG 2714
Qy 431 IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla 450
Db 2715 ATTGCAACAGAGCAATAGAAATATATAGGACAGTTGTCTTTGACCCAGGAAGAA 2774
Qy 451 PheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla 470
Db 2775 TTTGAATCAATGATGTTGAAATTTGTATGGACCTTACAGGAATTTCTGTGCAAGAGGCA 2834

Qy 471 GlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAla 490
Db 2835 CACATCTATGGAATTTACTTTTAGTATCTCACAAAGCAATTTATGTAATTTTCTCTATGCCGT 2894
Qy 491 GlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluLysMetPhe 510
Db 2895 TGTTTTCGATTTGGTGCATATCTCATTTGATGATGAGCATATCGCTTCCAGAGATGTTATT 2954
Qy 511 IleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValLeuAla 530
Db 2955 CTGGTGTTTTCTGCAATTTGTTTGGTGCAGTGGCTCTAGGACATGCCAGTTCATTTGCT 3014
Qy 531 ProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuGluLysLys 550
Db 3015 CCAGCATATGCTAAAGCTTAAGCTGTCTCAGCCCACTTATTCAATGCTGTTTGAAGACAA 3074
Qy 551 ProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGluGlyAsnLeu 570
Db 3075 CTTCTGATTTGACAGCTACAGTGAAGAGGGGCTGAAGCTGATAAATTTGAAGGAATATA 3134
Qy 571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly 590
Db 3135 ACATTTAATGAAGTCTGTCTCAACTATCCACCCCGAGCAAACTGCTCCAGTGTCTCAGGG 3194
Qy 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly 610
Db 3195 CTGAGCTTGGAGGTGAGAAAGCCCGACACTAGCCCTGTTGGCGGACAGTGGCTGTGG 3254
Qy 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
Db 3255 AAGACACGGTGTCTCAGCTCTCTGGAGCGGTCTTACGACCCCTTGGCGGGACAGTGTCT 3314
Qy 631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArgSerGlnIleAlaIle 650
Db 3315 CTCGATGTGCAAGAGCAAGAACTCAATGTCTCAGTGGCTCAGAGCTCAACTCCGAATC 3374
Qy 651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp 670
Db 3375 GTGCTCAGGAGCTTATCTCTATTGACTGCAGCAATTCGAGAGATATTGCTTATGGAG 3434
Qy 671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis 690
Db 3435 AACAGCCGGTGTATCATCAGGATGAAATTTGAGTGCAGCCAAAGCTGCCAACATACAT 3494
Qy 691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln 710
Db 3495 CTTTCATCGAGAGCTTACCCCAAAATATGAAACAGAGTGGAGATAGGGGACTCAG 3554
Qy 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
Db 3555 CTCTCAGGAGGTCAAAAACAGAGGATTTCTATTGCCAGAGCCCTCATCAGACAACTCAA 3614
Qy 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLysValValGln 750
Db 3615 ATCTCTCTGTGGATGAAGCTACATCAGCTCTGGATACCTGAAGTGAAGAGTTGTCCAA 3674
Qy 751 HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer 770
Db 3675 GAAGCCCTGGACAAAGCCAGAGAGGCCGACCTGCTGCTGATTTGCTCACCGCTGTCC 3734
Qy 771 AlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGluGlnGly 790
Db 3735 ACCATCCAGATGTCAGACTTAATAGTGTGTTTCAGAAATGGAGAGTCAAGAGCATGGC 3794
Qy 791 ThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
Db 3795 ACGCATCAGCAGCTCTCTGGCACAGAAAGCATCTATTTTTCAATGCTCAGTGTCCAGGCT 3854
RESULT 11
US-10-101-433A-1
; Sequence 1, Application US/10101433A
; Publication No. US20030119726A1

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; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara
; APPLICANT: Crespi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00367/70019
; CURRENT APPLICATION NUMBER: US/10/101.433A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277,095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3852
; TYPE: DNA
; ORGANISM: Macaca mulatta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3852)
US-10-101-433A-1

Alignment Scores:
Pred. No.: 2,13e-232 Length: 3852
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best Local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 15 Gaps: 5

US-09-873-409-2 (1-812) x US-10-101-433A-1 (1-3852)

Qy 2 ValAspGluAsnAspIleAArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1366 GTTCATGGACAGGATATTAGGACCAATAAAGCTAAGGTTTCTACGGAAATCATCGGTGTG 1425

Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1426 GTGAGTCAGAAACCTGTATTGTTTGGCCACACGATAGCTGAAACATTCGCTATGTCGT 1485

Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1486 GAAGATGTCACCATGGATGAGATTGAGAAAGCTGCTCAAGGAGCCANTGCTATGACTTT 1545

Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1546 ATCATGAAACTGGCTTCAGAAATTTTGACACCTGTTGGAGAGAGAGGGGCCAGTCAGT 1605

Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaAArgAlaLeuValArgAsnProLysIleLeu 101
Db 1606 GGTGGGACAGACGACAGATCGCATTCGACGTGCTGTTGCGAACCCACAGATCCTC 1665

Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1666 CTGCTGGACAGGCGCACTGACGCTTGGACACACAGAAAGTGAAGCAGTGGTTCAGTGGCT 1725

Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 1726 CTGTAAGGCCAGAAAGGTGGACCAACATTTGTATAGCTCATGCTTTGTTGTACCGTT 1785

Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1786 CGTAATGCCAGCGTCATCGCTGGTTTCGATGATGCGTTCATTTGGAGAGAAAGAAATCAT 1845

Qy 162 AlAGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle--- 180
Db 1846 GATGAGCTCANAAGAGAGAGGAGGATTTACTTCAAACTTGTCAAATGCAGACAGCAGGA 1905

Qy 181 -----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191
Db 1906 AATGAAATTGAATTAGAAATGTCAGCTGATGATCCAAAGTGAATGATACCTTGAA 1965

Qy 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206
Db 1966 ATGCTTTCATGATTCAGATTCGATTCCTAATAGAAAAAGATCCACTCGTAGAGGTGC 2025

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QY 566 CysGluGluValAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspVal 585
DB 3100 TTGGAAAGGAAATGTCATTAATGAATGTTGTTTCAACATATATCCACCCGAGCTGGACATC 3159
QY 586 PheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyThrValAlaPheValGly 605
DB 3160 CCAGTCTTCAGGAGCTGAGCCCTGGAGTGAAGAGGAGGCGAGACATGGCCCTGGTGGGC 3219
QY 606 SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuArgLeuTyrAspProVal 625
DB 3220 AGCAGTGGCTGTGGGAAGACAGCCGGTGTCCAGCTCTGGAGCGGTTCATGACCCCTTG 3279
QY 626 GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArg 645
DB 3280 GCGGGGAAAGTGTCTTGACGGCAAGAAATAAAGCACTGAATGTTTCAAGTGGCTCCGA 3339
QY 646 SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
DB 3340 GCACACTGGGCATCTGTGCCAGAGCCCATCTCTTTGACTGACGATTAAGTGAAC 3399
QY 666 IleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAsn 685
DB 3400 ATTGCTTATGAGACACACAGCCGGTGTGTCAAGGAAGAGATCTGTGGGCGAGCAAG 3459
QY 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
DB 3460 GAGGCCAATATACAGCCCTTCATGAGTCACTGCTTAATATATAGCACGAGTAGGA 3519
QY 706 LeuLysGlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
DB 3520 GACAAAGGAATCAGCTCTCTGGTGGCCAGAAACAGCATGCCATAGCTGTGGCCCTT 3579
QY 726 LeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnSer 745
DB 3580 GTTAGACAGCCCTCATATTTTGTCTTTGGATGAAGCCACATCAGCTCTGGATACAGAAAT 3639
QY 746 GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
DB 3640 GAAAGGTTGTCCAGAGCCCTTGACAAAGCCAGAGAGCGGCTACCTGCTGATGTGAT 3699
QY 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisArgLys 785
DB 3700 GCTACCGCGCTGTCCACCATCCAGATGCGAGACTTAATATGTTGTTCAGAAATGCGCA 3759
QY 786 IleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeu 805
DB 3760 GTCAAGGAGCAGCGCACACATCAGCAGCTGTCTGGCAGAGGCACTATTTTCAATG 3819
QY 806 ValAsnAlaGlnSer 810
DB 3820 GTCAGTGTCCAGGCT 3834

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RESULT 12

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US-10-619-359A-1
; Sequence 1, Application US/10619359A
; Publication No. US20040077000A1
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES E.
; TITLE OR INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307.70020.US
; CURRENT APPLICATION NUMBER: US/10/619,359A
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 09/672,810
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1

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Alignment Scores:

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Pred. No.: 2,42e-232 Length: 4186
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best Local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 17 Gaps: 5

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US-09-873-409-2 (1-812) x US-10-619-359A-1 (1-4186)

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QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1456 GTTGATGACAGGATATTAGGACCATAAACGTAGGTTTCTACGGGAATATCATCGGTGTG 1515
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1516 GTGAGTCAAGAACCTGTATTGTTGCCACACGATAGCTGAAACATTCGCTATGCTGT 1575
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
DB 1576 GAAGATGTCACCATGATGAGATTGAGAAAGCTGTCAAGGAAGCCCAATGCCCTATGACTT 1635
QY 62 IleMetGluPhePheAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
DB 1636 ATCATGAACCTGCTCAGAAATTTGACACCTGTTGTGAGAGAGAGGGCCGAGCTGAGT 1695
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 1696 CGTGGGCGCAAGACAGAGGATGCCATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1755
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
DB 1756 CTGCTGAGAGGCGCCAGCTCAGCTTGGACACAGAAAGTGAAGCAGTGTTCAGTGGCT 1815
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
DB 1816 CTGGATAAGGCAGAAAGGTCGGACCACTTGTGATAGCTCATCGTTGTCTACGGTT 1875
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1876 CGTAATGCCAGCTCATCGCTGTTTCGATGATGAGTCATTGTGGAGAAAGGAATCAT 1935
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle--- 180
DB 1936 GATGAGCTCATGAAGAGAGAGGCACTTTACTTCAAACTTGTCAACAATGCAGACAGCA 1995
QY 181 -----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191
DB 1996 AATGAATTTGAATTAAGAAATGACAGCTGATCAATCCAAAAGTGAATTTGATACCTTGA 2055
QY 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206
DB 2056 ATGCTTTCACATGATTCAGGATCCAGTCTAATAGAAAAGAGTCCACTCGTAGGATGTC 2115
QY 207 LysSerIleLysSerAspPheIleAspLysAlaGluSerThrGlnSerLysGluIle 226
DB 2116 CGTGGATCACAAGGCCAA-----GACAGAAAGCTTAGTACCAGAGGCTCTGGATGA 2169
QY 227 SerLeuProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTrpProPhe 246
DB 2170 AGTATACCTCCAGTTTCCTTTTGGAGGATTAAGAGCTAAATTTAACTGAGTGGCTTAT 2229
QY 247 ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle 266
DB 2230 TTGTGTTGTGTGTTATTTTGTGCCATTATAAATGAGGCTCTGCAACCAAGCAATTGCA 2289

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QY 267 IlePheAlaIysIleThrMetPhe---GlyAsnAspAspLysThrLeuLysHis 285
 Db 2290 ATATTTTCARAAGATTATAGGATTTTACAGAATATGATGCGCAAAACAAACGACAG 2349
 QY 286 AspaAGluIleIleThrMetIlePheValIleLeuGlyValIleCysPheValSerIle 305
 Db 2350 AATAGTAATCTGTTTCTCACTATGTTTCTAGTCTTGGAAATGTTCTTTTATTACATT 2409
 QY 306 PheMetGlnGlyLeuPheThrGlyArgAlaGlyLeuIleLeuThrMetArgLeuArgHis 325
 Db 2410 TTCCTTCAGGCTTCACATTTGGCAAGCTGGAGATCTCCACCAAGCGGCTCCGATAC 2469
 QY 326 LeuAlaPheLysAlaMetLeuIleGlnAspIleAlaIlePheAspGluLysGluAsnSer 345
 Db 2470 ATGTTTTCAGATCCATCTCAGACAGATGAGCTGTTTGTATGACCTTAAACACACC 2529
 QY 346 ThrGlyGlyLeuThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
 Db 2530 ACTGAGCATTTGACTACCAAGCTCGCCATCATCTGCTCAAGTTAAAGGGGCTATAGGT 2589
 QY 366 SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385
 Db 2590 TCCAGCTTCGTATTAATACCAAGATATACCAATCTTGGACAGGATTAATATATACC 2649
 QY 386 PheIleIleGlyThrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
 Db 2650 TTAATCTATGTTGGCAACGACATGTTACTCTTAGCAATTTGACCATCATTTGCAATA 2709
 QY 406 ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
 Db 2710 GCAGAGTGTGTAATGAATGTTGCTGACAGCAAGCACTGAAGATAGAGAAAGACTA 2769
 QY 426 LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445
 Db 2770 GAAGTGCTGGGAAGATCGCTACTGAAGCAATAGAAAACCTCCGAACCTGTTGTTCTTTG 2829
 QY 446 ThrArgGluLysAlaPheGluMetThrGluGluMetLeuGlnThrGlnHisArgAsn 465
 Db 2830 ACTCAGGACGAGAGTTTGAACATATGATGATCAGAGTTGCGAGTACCATCAGCAAC 2889
 QY 466 ThrSerLysLysAlaGlnIleIleGlySerCysIleAlaPheSerHisAlaPheIleIle 485
 Db 2890 TCTTTGAGGAAGACACACATCTTTGGATACGTTTCTTCCACGACGCAATCATGTAT 2949
 QY 486 PheAlaIleAlaAlaGlyPheArgPheGlyAlaIleLeuIleGlnAlaGlyArgMetThr 505
 Db 2950 TTTTCTATGCTGGATGTTTCCGTTTGGAGCCTACTTGGTGGCACATAGTCTCATGAGC 3009
 QY 506 ProGluGlyMetPheIleValPheThrAlaIleAlaIleAlaIleAlaIleGlyLys 525
 Db 3010 TTTGAGGATGTTCTGTTAGTATTTTACGCTGTTGCTGTCATGCGCGTGGGCA 3069
 QY 526 ThrLeuValLeuAlaProGluIleSerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545
 Db 3070 GTCAGTTTCATTTGCTCTGACTATGCCAAAGCCAAAGTATATCAGGAGCCCATCATCATG 3129
 QY 546 LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565
 Db 3130 ATCATTGAAAACCCCTTGAATGACAGCTACAGCAGAGAGCCCTAAGCCGAAACACA 3189
 QY 566 CysGluGlyAsnLeuGluPheArgGluValSerPhePheIleProCysArgProAspVal 585
 Db 3190 TTGGAAGGAATGTCACATTTAATGAAGTTGTTTCAACTATCCACCCGCTGGACATC 3249
 QY 586 PheIleLeuArgGlyLeuSerLeuIleGluArgGlyLysThrValAlaPheValGly 605
 Db 3250 CCAGTGCTTCAGGGCTGAGCTGGAAGTGAAGAGGGCCAGAGCGCTGGCCCTGGTGGC 3309
 QY 606 SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuIleAspProVal 625
 Db 3310 AGCAGTGCTGGGAAGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3369

QY 626 GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTTPLeuArg 645
 Db 3370 GCGGGGAAGTCTGCTTACGCGCAAGAAATTAACCACTGAATGTTTCTAGTGGCTCCGA 3429
 QY 646 SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
 Db 3430 GCACACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3489
 QY 666 IleAlaIleGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsn 685
 Db 3490 ATTGCTTATGGAGAACACCGCGGTGGTGTCTCAGAGAGAGATCTGTAGGGCGGCGCAAG 3549
 QY 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysIleThrGlnValGly 705
 Db 3550 GAGGCAATATATACGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3609
 QY 706 LeuLysGlyAlaGlnIleSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
 Db 3610 GACAAAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3669
 QY 726 LeuGlnLysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
 Db 3670 GTTAGACAGCTCATATTTTGTGTTTGGATGAAGCCACATCAGCTCTGGATACAGAAAGT 3729
 QY 746 GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
 Db 3730 GAAAGAGTTTGTCCAGAGCCCTGCGCAAGCCAGAGAGCGGTACCTGCTGCTGCTGCTGCT 3789
 QY 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
 Db 3790 GCTCAGCGCTGTCCACCATCCAGATGCGAGCTTAATAGTGTGTTTTCAGATGCGAGA 3849
 QY 786 IleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleThrPheLysLeu 805
 Db 3850 GTCAGAGCAGCGGACACATCAGCAGCTGCTGCGCACAGAAAGGCAATCTATTTTCAATG 3909
 QY 806 ValAsnAlaGlnSer 810
 Db 3910 GTCAGTGTCCAGCT 3924

RESULT 13
 US-10-619-359A-3
 ; Sequence 3, Application US/10619359A
 ; Publication No. US20040077000A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STOCKER, PENNY J.
 ; APPLICANT: STEINEL-CRESPI, DOROTHY T.
 ; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
 ; FILE REFERENCE: G00307.70020.US
 ; CURRENT APPLICATION NUMBER: US/10/619,359A
 ; CURRENT FILING DATE: 2003-07-14
 ; PRIOR APPLICATION NUMBER: US 60/156,921
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/158,818
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: US 09/672,910
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 4195
 ; TYPE: DNA
 ; ORGANISM: Macaca fascicularis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (100)...(3949)
 US-10-619-359A-3

Alignment Scores:
 Pred. No.: 2,42e-232 Length: 4195
 Score: 2441.00 Matches: 465
 Percent Similarity: 76.73% Conservative: 168

Best Local Similarity: 56.36%				Mismatches: 174			
Query Match: 59.84%				Indels: 18			
DB: 17				Gaps: 5			
US-09-873-409-2 (1-812) x US-10-619-359A-3 (1-4195)							
QY	2	ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal	21	QY	326	LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSer	345
DB	1465	GTGATGGACAGGATATTAGACCATTAAGCAAGTAAAGTTTCTACGGGAAATCATCGGTGTG	1524	DB	2479	ATGGTTTTCGGATCCATGCTCAGACAGGATGTGAGCTGGTTGATGACCTTAAACACACC	2538
QY	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg	41	QY	346	ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly	365
DB	1525	GTGAGTCAGGAACCTGTATTGTTGGCCACCATAGCTGAAACCATTCGCTATGTGCT	1584	DB	2539	ACTGGAGCATTTGACTACCAAGGCTCGCCATGATGTCTTCAAGTTTAAAGGGCTTATAGGT	2598
QY	42	AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe	61	QY	366	SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer	385
DB	1585	GAAGATGTCACATGATGAGATGAGAAAGCTGTCAAGCAAGCCCAATGCTATGACTTT	1644	DB	2599	TCAGGCTTGTCTATTAATACCCAGATATAGCAATCTTTGGACAGGAATATATATATCC	2658
QY	62	IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer	81	QY	386	PheIleTyrGlyTyrPheLumMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal	405
DB	1645	ATCATGAACTGCTCAGAAATTTGACCCCTGGTTGGAGAGAGGGGCCCGAGTGT	1704	DB	2659	TTAATCTATGTTGGCAACTGACACTGTCTACTCTTAGCAATTTGTACCCATCATTCGAATA	2718
QY	82	GlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu	101	QY	406	ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu	425
DB	1705	GGTGGCAGAAAGCAGAGATCGCCATTCACGCTGCTGCTGCAACCCCAAGATCCTC	1764	DB	2719	GCAGGAGTTTGTGAATGAAATGTTGTCTGGCAGACACTGAAAGATAGAAAGAACTA	2778
QY	102	IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla	121	QY	426	LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu	445
DB	1765	CTGCTGACGAGGCCAGCTCAGCCCTTGGACACAGAAAGTGAAGCAGTGTTCAGGTGGCT	1824	DB	2779	GAAGGTGCTGGGAAGATCGCTACTGAGCAATAGAAACTTCCGAACCTGTTGTTCTTTG	2838
QY	122	LeuGluLysAlaSerLysGlyArgThrThrIleValAlaAlaHisArgLeuSerThrIle	141	QY	446	ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn	465
DB	1825	CTGGATAAGGCCAGAAAGGTGCGACCAACCATTTGTGATAGCTCATCGTTTGTCTACGGTT	1884	DB	2839	ACTCAGGACGACAAAGTTCGAACATATGATGATCAGAGTTTGCAGGTACCATACAGAAC	2898
QY	142	ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis	161	QY	466	ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr	485
DB	1885	CGTAATGCCAGCTGTCGCTGCTGCTGATGAGTGGAGTCAATTCGAGAAAGCAATCAT	1944	DB	2899	TCCTTGGAGAAAGCACACATCTTTGGAATCAGCTTTCCTTCCAGCAGCAATGATGAT	2958
QY	162	AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle---	180	QY	486	PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr	505
DB	1945	GATGAGCTCATGAAGAGAAAGCAATTTACTTCAAACTTGTCAAATGCGACAGCAGGA	2004	DB	2959	TTTCTCTATGCTGGATGTTTCCGGTTTGGAGCCTACTTGGTGGCACATAGTCTCATGAGC	3018
QY	181	-----LysLysAlaAspGlu-----GlnMetGluSerMetThr	191	QY	506	ProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLys	525
DB	2005	AATGAAATGAAATAGAAAATGCGCTGATGAATCCAAAAGTGAAATTCATCTGGAA	2064	DB	3019	TTTGAGGATGTTCTGTTAGTATTTTCAGCTGTGTTCTTGGTGCCATGCGCGGGGCAA	3078
QY	192	TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal	206	QY	526	ThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAla	545
DB	2065	ATGCTCTCAGATNTTCAGGATCCAGTCTAATAAGAAAGATTCACCTCGTAGGAGTGC	2124	DB	3079	GTGAGTTCATTTGCTCTCTGACTATGCCAAGCCAAAGTATCAGCAGCCCATCATCATG	3138
QY	207	LysSerIleLysSerAspPheIleAspLysAlaGluSerThrGlnSerLysGluIle	226	QY	546	LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr	565
DB	2125	CGTGGATCACAGGCCAA-----GACAGAAAGCTTAGTACCAAGAGGCTCTGGATGAA	2178	DB	3139	ATCATTGAAAGAAACCCCTTTGATTGACAGCTACAGCACAGAAAGGCTTAAAGCCGAACA	3198
QY	227	SerLeuProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPhe	246	QY	566	CysGluGlyAsnLeuLeuGluPheArgGluValSerPhePheTyrProCysArgProAspVal	585
DB	2179	AGTATACCTCCAGTTTCTCTTTGGAGGATATGAAGCTAAATTTAACTAGTGGCTTAT	2238	DB	3199	TTGGAAGGAANTGCACATTTAATGAAGTTGTATTCAACTATCCACCCGACTGGACATC	3258
QY	247	ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle	266	QY	586	PheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGly	605
DB	2239	TTTGTTGTTGGTATTTTGTGGCATTAATAATGAGGCTGCAACACCATTTGCGATA	2298	DB	3259	CCAGTGTCTCAGGGGCTGAGCCTCGAAAGTGAAGAGGGCCAGACGCTGGCCCTGGTGGGC	3318
QY	267	IlePheAlaLysIleIleThrMetPhe---GlyAsnAsnAspLysThrThrLeuLysHis	285	QY	606	SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProVal	625
DB	2299	ATATTTTCAAGATTATAGGATTTTTCAGAAATATGATGATGCGCAAAACAGACAG	2358	DB	3319	AGCAGTGGCTGTGGAGAGAGACCGGTGCTCCAGCTTCTTGGAGCGGTTCTATGACCCCTTG	3378
QY	286	AspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr	305	QY	626	GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArg	645
DB	2359	AATAGTAACCTGTTTTCATATGTTTCTAGTCCCTTGGAAATGTTTCTTTTATTCATTT	2418	DB	3379	CGCGGGAAGTGTCTGTGACGGCAAGAAATAAAGCAACTGAAATGTTTCAGTGGCTCGCA	3438
QY	306	PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis	325	QY	646	SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn	665
DB	2419	TTCTTTCAGGGCTTCACATTTGGCAAGCTGGAGAGATCCTCACCAAGCGGCTCGGATAC	2478	DB	3439	GCACACCTGGGCATCGTGTCCAGGAGCCCATCTCTTTTGTAGTCAGCATTTAGTGAGAAC	3498
QY	306	PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis	325	QY	666	IleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsn	685
DB	2419	TTCTTTCAGGGCTTCACATTTGGCAAGCTGGAGAGATCCTCACCAAGCGGCTCGGATAC	2478	DB	3499	ATTGCCTATGAGACAAACAGCGGGTGTGTCCACAGGAAGAGATCGTGGAGCGGACCAAG	3558

Qy 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
Db 3559 GAGCCCAATATACAGCGCTTCAATGAGTCACTGCTTAATAATATACACAGATAGGA 3618
Qy 706 LeuLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
Db 3619 GACAAGAGAACTCAGCTCTCTGTGGTGGCCAGAAAACAGCCGATTCGCATAGCTGGTGCCTT 3678
Qy 726 LeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
Db 3679 GTTAGACAGCGCTCTATTTTCTTTGATGAGCCACATCAGCTCTGGATACGAAGT 3738
Qy 746 GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
Db 3739 GAAAAGGTGTTCACAAAGCCCTGCACAAAGCCAGAGAGCCGCTACCTGCTGATTTGAT 3798
Qy 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
Db 3799 GCTCAGCGCTGTCCACCATCCAGATGCAGACTTAATAGTGGTTCAGATGGCGGA 3858
Qy 786 IleLysGlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleLysPheLysLeu 805
Db 3859 GTCAAGGAGCAGCGCCACACATCACAGCTGCTGCCACAGAAAGCACTATTTTCAATG 3918
Qy 806 ValAsnAlaGlnSer 810
Db 3919 GTCAGTGTCCAGGCT 3933
RESULT 14
US-09-769-097-1
; Sequence 1, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feild
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: ENCODING RAT MDRIA AND SCREENING METHODS THEREOF
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4369
; TYPE: DNA
; ORGANISM: RATTUS RATTUS
US-09-769-097-1
Alignment Scores:
Pred. No.: 2,58e-232 Length: 4369
Score: 2441.00 Matches: 470
Percent Similarity: 77.04% Conservative: 164
Best Local Similarity: 57.11% Mismatches: 175
Query Match: 59.84% Indels: 14
DB: 9 Gaps: 5
US-09-873-409-2 (1-812) x US-09-769-097-1 (1-4369)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1684 ATCCAGCGACAGGACATCAGACCATCAATGTGAGGTATCTCGCGGAAATCATTTGGGGTG 1743
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnIleLysTyrGlyArg 41

Db 1744 GTGAGTCAGGAACCCGCTGCTGTTTCCACCAACAATTCGCGAAAAACATTCGCTATGCGCGA 1803
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1804 GAAAAGCTCACCATGATGATAGTAGAAGCTGTCAAGGAAGCCATGCCATGATTTTC 1863
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGlyLysGlyAlaGlnMetSer 81
Db 1864 ATCATGAAACTGCCCCACAAATTTGACACCTGTTGTTGTTGAGAGAGGGCGCAGCTGAT 1923
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1924 GGGGGACAAACAGAGGATCCCATTCGCCGGGCCCTGTCCGCAACCCCAAGATCCCT 1983
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1984 TTGTTGATGAGCCACAGCTCAGCTTGGACACAGAAAGCGGCGGTGTTTCAGGCCGCT 2043
Qy 122 LeuGlyLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 2044 CTGGATTAAGCTTAGAAGCGCGACCCATTTGTGATAGCTCACCGCTGTGCTACAGTT 2103
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 2104 CGCAATGCTGACGTCATTCCTGTTGATGCTGTTGTTGATGCTGAGGAGCAAGAAATCAT 2163
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln 178
Db 2164 GATGAGCTCATGAGAGAGAAAGAAATTTACTTCAAACTTGTCTGATGACTCAGACAGCA 2223
Qy 179 ---AspIleLysLysAlaAspGluGlnMetGluSer 191
Db 2224 AATGAAATTTGAATTAGGAATGAGCTTGTGAATCTTAAGACGGAATGATTAATGTGGAC 2283
Qy 192 TyrSerThrGluArgLysThrAsnSerLeu 209
Db 2284 ATGTCTTCAAAAGATTCGGGATCCAGTCTATAAGAGAAAGATCACTCGCAAAAGCATC 2343
Qy 210 LysSerAspPheIleAspLysAlaGluGluSerThr 228
Db 2344 CTGGGCCCATGATGATCAAGCGGGAACTTGACCAAGAGGCTCTGGATGACGACGTA 2403
Qy 229 ProGluValSerLeuLysIleLysLysLeuAsnLysProGluTrpProPheValVal 248
Db 2404 CTTCCAGCTTCTTTTGGCGGATCTCTGAAGTTGAATTCAACTGGAATGGCTTAATTTG 2463
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2464 GTTGGTGTATTTGTGCCATAATAATGAGGCTTGCAACCCAGCATTCCTCCATAATATT 2523
Qy 269 AlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeu 287
Db 2524 TCBAAGTTGTAGGGGTTTTTACAAAAAATGACACCCCTGAAATCCAGCGGAGAAACAGC 2583
Qy 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
Db 2584 AACTTGTCTTTCTTATTGTTCTGATCCTTGGGATCATCTCTTTTATTACGTTTTTCTTT 2643
Qy 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2644 CAGGGCTTCACATTTGGCAAGCTCGAGAGATCTCTCACCAGCGACTCCGATACATGGTC 2703
Qy 328 PheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
Db 2704 TTCAAAATCCATGCTGAGACAGGACATAAGCTGTGTTGATGCCCTTAAACCAACCAACAG 2763
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 2764 GGGCTGACCCAGGCTTCCCAATGCGCTGCTCAAGTGAAGGGGCTACAGGGTCTAGG 2823
Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2824 CTTGCTGTTATTATCCAGAAACATAGCAAAATCTTGGGACAGGATCATCATATCCCTGATC 2883

QY 388 TyrGlyThrProGluMetThrPheLeuLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2884 TACGGCTGGCAATTTGACCTTTTACTCTTCTAGCAATTTGTTCCCATCATCTCTATAGCAGGA 2943
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
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QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 3004 TCTGGGAATGCTCTACAGAGCAATTTGAAACTTTTCGCACTGCTCTCTTTGACTCGG 3063
QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3064 GAGCAGAGTTTGAACATAATGATGATGCCAGAGCTTCAGATACCATACAGAAATGCTTTG 3123
QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
Db 3124 AAGAAAGCGCAGCTCTTTGGATCACTTTCTCTTCCAGCCCATGATGATTTCTCC 3183
QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 3184 TATGCTGCTTTGTTCCGGTTGATGCTACTTGTGGCAGGAACTCATGACATTTGAA 3243
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3244 AATGTTCTGTATTCTCAGCTATTGTTCTTGTGGTCCATGCGAGTGGCGGCGGTCACT 3303
QY 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3304 TCATTCGCTCTGACTACCGGAAGCCAAAGTCTCGGCATCCCATCATCATCAGGATCAT 3363
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3364 GAGAAATCCCTGAGATTGACAGCTACAGCAGGAGGCTTGAAGCCTAATATGTTGAA 3423
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
Db 3424 GGAATGTGAATTTAATGAGFCATGTTCAACTATCCACCCGACCCCACTCCCGAGTG 3483
QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3484 CTTCAGGGCTGAGCTTAGAGTGAGAGAGGGCAGACCTGGCCCTCTGCGGACAGCT 3543
QY 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
Db 3544 GGCCTGCGGAAGAGTACAGTGTCTCCAGCTGCTTGAAGCGCTTCTATGACCCCATGCGCGGA 3603
QY 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArgSerGln 647
Db 3604 ACAGTGTTTCTAGATGGCAAGAAATAAAGCACTCAATGTCAGTGGCTCCGCCCCAC 3663
QY 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3664 CTGGGCATTTGTCCAGGAGCCCATCTCTGTTGACTGCAGCATCCCGAGAACATTTGCC 3723
QY 668 TyrGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsnAlaAla 687
Db 3724 TACGGAGACAACAGCGCTGTCTGCTGCTCATAGGAGATCTGAAGGAGCCCAAGAGGCC 3783
QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 3784 AACATCCACCGTTCATCGACTCACTGCTGCTGAGAAATACACACAGAGTGGAGACAAA 3843
QY 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
Db 3844 GGGACTCACTGTGCGGCGGAGAGAGCAGCGCATCGCCATCGCGCGGCCCTCTGTCAGA 3903
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 3904 CAGCCTCACATCTTCTTGTGATGAGCGCATCAGCTCTGATACGAGAGTGAAG 3963

QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3964 GTGCTCCAGGAGCGCTCGACAAAGCCAGGAGCCGCACTGCTGTGTATCGCGCAC 4023
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4024 CGCTGTCCACCATCCAGACCGCAGACTGTATCGTGTGATTTCAGAACGGCCAGGTCAAG 4083
QY 788 GluGlnGlyThrHisGlnGlnLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
Db 4084 GAGCAGCGCACCCACAGCAGCTGTGCCCCAGAAAGCACTATTTCGTATGTCAGT 4143
QY 808 AlaGlnSer 810
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RESULT 15
US-09-769-097-3
; Sequence 3, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feild
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: ENCODING RAT MDRLA AND SCREENING METHODS THEREOF
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: RATTUS RATTUS
US-09-769-097-3

Alignment Scores:
Pred. No.: 2,63e-232 Length: 4425
Score: 2441.00 Matches: 470
Percent Similarity: 77.04% Conservative: 164
Best Local Similarity: 57.11% Mismatches: 175
Query Match: 59.84% Indels: 14
Gaps: 5

US-09-873-409-2 (1-812) x US-09-769-097-3 (1-4425)

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QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1744 GTGAGTCAGGAACCGTGTCTTTCGCCACCAATTCGCGAAACATTCGCTATGCGCGA 1803
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1804 GAAACGTCACCATGTGATGATAGAGAACTGTCTAGGAGCAATCCCTATGATTTTC 1863
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1864 ATCATGAACTGCCCAAAATTTGACACCTGTTGAGAGAGAGGGCGCAGCTGAGT 1923
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101

Db 1924 GGGGACAGAAACAGAGGATCGCCATTGGCCCGGCCCTGGTCCGCAACCCCAAGATCCCTT 1983
Qy 102 ILeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1984 TTGTGTGATCAGGCGCCAGTTCAGGCTTTGGACACAGAAAGGAGCCGCTGGTTCAGGCGCGT 2043
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaAlaHisArgLeuSerThrIle 141
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Qy 192 TySerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerValLysSerIle 209
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Db 2464 GTTGTGTATTTTGTGCCATAATAAATGGAGGCTTGCAACACGACATTTCTCCATAATATT 2523
Qy 269 AlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeu---LysHisAspAla 287
Db 2524 TCAGAGCTGTAGCGGCTTTTACAAAAAATGACACCCCTCAATCCAGCGGCGAGACAGC 2583
Qy 288 GluIleTySerMetIlePheValIleLeuGlyValIleCysPheValSerTyPheMet 307
Db 2584 AACTGTGTCTTATTTGCTTCTGATCTCTGGATCATCTTTCATAGCTTTTCCCT 2643
Qy 308 GlnGlyLeuPheTyGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2644 CAGGCTTCATTTGGCAAGCTGGAGAGATCTCACCAGGAGCTCCGATACATGGTC 2703
Qy 328 PheLysAlaMetLeuTyGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
Db 2704 TTCAAATCCATCTGACAGACGACATAGCTGTGTTGATGACCTTAAACACACACAGGA 2763
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 2764 GCGCTGACCCAGGCTTGCCATGACGCTGCTCAAGTGAAGGGGCTACAGGCTCTAGG 2823
Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2824 CTTCCTGTTATATCCAGACATAGCAAAATCTTGGACAGGACATCATATCCCTGATC 2883
Qy 388 TyGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2884 TACGCTGGCAATTCAGACTTTTACTCTAGCAATTTGTTCCATCTTGTATAGCAGGA 2943
Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnLeuLysHis 427
Db 2944 GTGTTGAATGAATAATGTTGTCTGGACAGCGCTGAAAGATAGAAAGGAAGTGAAGGT 3003
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuAsnIleArgThrIleValSerLeuThrArg 447
Db 3004 TCTGGAGAGATCGCTACAGAGCAATTGAAACATTTTCGACTGTCTCTTTGACTCGG 3063

Qy 448 GluLysAlaPheGluGlnMetTyGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
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Db 3124 AAGAAAGCGCAGCTCTTTGGATCATCTTCTCCTTACCAGGCCATGATGATTCTCC 3183
Qy 488 TyAlaAlaGlyPheArgPheGlyAlaTyIleuIleGlnAlaGlyArgMetThrProGlu 507
Db 3184 TATGCTGTGTTTCCGCTTGTATCCCTTGTGGTGGCAGCAAACTCATGACATTTGAA 3243
Qy 508 GlyMetPheIleValPheThrAlaIleAlaTyGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3244 ANTGTCTGTAGTATTCTCAGTATTCTTTGGTGCCATGGCAGTGGGGGAGGTCAGT 3303
Qy 528 ValLeuAlaProGluTyThrSerLysLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3304 TCATTGCTCTCTGACTAGCGAAAGCAAGTCTCGGCATCCCATCATCATCAGGATCAT 3363
Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3364 GAGAAATCCCTGACATTTGACAGCTACAGCAGGAGGGCTTGAAGCCATATATGTTGAA 3423
Qy 568 GlyAsnLeuGluPheArgGluValSerPheTyProCysArgProAspValPheIle 587
Db 3424 GGAATGTGAATTTAATGGAGTTCATGTCAACTATCCACCCGACCCCAACATCCAGTG 3483
Qy 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3484 CTTGAGGCTGAGCTAGAGGTGAAGAGCGCAGAGCTGGCCCTCGTGGGAGCAGT 3543
Qy 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyAspProValGlnGly 627
Db 3544 GCGTCGGGAGAGTACAGTGTGTCAGCTGTGTGAGCGCTTCTATGACCCCATGCGCCGA 3603
Qy 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuLeuAsnValGlnTrpLeuArgSerGln 647
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Qy 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3664 CTGGCATTTGTCTCCAGGAGCCCATCTCTGTTGACTGCGAGCATGCGCGAGAACTTGC 3723
Qy 668 TyGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAlaAla 687
Db 3724 TACGAGACACAGCCGCTGTGTCTCATAGGAGATCGTGAAGGCGAGCCCAAGAGGCC 3783
Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyAsnThrGlnValGlyLeuLys 707
Db 3784 AACATCCACCATTCATCGACTCATGCTGAGAAATACACACAGAGTGGGAGACAA 3843
Qy 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
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Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4024 CCGCTGTCCCATCCAGAACCGACACTTGATGTGGTGTGATTCAGNACCGCCAGGTCAAG 4083
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Qy 808 AlaGlnSer 810
Db 4144 GTGCAGGCT 4152

Search completed: June 25, 2004, 03:51:13
Job time : 994 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2004, 23:38:48 ; Search time 167 Seconds

(without alignments)
2698.324 Million cell updates/sec

Title: US-09-873-409-2

Perfect score: 4079

Sequence: 1 MYDENDIRALNRYHRDHIG.....QELLNRDIYFKLVNAQSVQ 812

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09873409/runat_24062004_153026_16687/app_query.fasta_1.967
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A-COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A-COMB.seq.*
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- 5: /cgn2_6/ptodata/2/ina/PTUS-COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2465.5	60.4	3924	4	US-09-023-655-1168 Sequence 1168, Ap
2	2465.5	60.4	3924	4	US-09-762-195-2 Sequence 2, Appli
3	2441	59.8	4186	4	US-09-672-810-1 Sequence 1, Appli
4	2441	59.8	4195	4	US-09-672-810-3 Sequence 3, Appli
5	2436	59.7	3988	4	US-09-762-195-1 Sequence 1, Appli
6	2436	59.7	4264	2	US-08-784-649A-1 Sequence 1, Appli
7	2436	59.7	4264	2	US-08-784-649A-5 Sequence 5, Appli
8	2436	59.7	4646	1	US-08-181-471-2 Sequence 2, Appli
9	2436	59.7	4646	4	US-09-023-655-1167 Patent No. 5206352
10	2436	59.7	4669	6	5206352-3 Sequence 1167, Ap
11	2436	59.7	8505	2	US-08-793-610-5 Sequence 5, Appli
12	2436	59.7	8630	4	US-09-306-417-1 Sequence 1, Appli

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14	2436	59.7	9318	2	US-08-793-610-6 Sequence 6, Appli
15	2413.5	59.2	4233	3	US-09-120-512-1 Sequence 1, Appli
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18	2412	59.1	4669	4	US-09-316-167-1 Sequence 1, Appli
19	2412	59.1	4669	4	US-09-397-233-1 Sequence 1, Appli
20	2397	58.8	4669	2	US-08-583-276-18 Sequence 18, Appli
21	2280	55.9	2726	1	US-08-461-823-1 Sequence 1, Appli
22	1894	41.5	4175	4	US-09-749-340-3 Sequence 3, Appli
23	1690.5	41.4	4002	2	US-08-996-545-1 Sequence 1, Appli
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28	1661	40.7	4047	2	US-08-612-734B-1 Sequence 1, Appli
29	1618	39.7	4800	2	US-08-612-734B-3 Sequence 3, Appli
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31	1570.5	38.5	3924	1	US-08-395-246C-1 Sequence 1, Appli
32	1538.5	37.7	2681	4	US-09-749-340-8 Sequence 8, Appli
33	1474	36.1	4224	1	US-08-612-521-1 Sequence 1, Appli
34	1255.5	30.8	3909	1	US-08-232-537-1 Sequence 1, Appli
35	1223.5	30.0	3924	2	US-08-996-644-3 Sequence 3, Appli
36	1223.5	30.0	3924	3	US-09-352-552-3 Sequence 3, Appli
37	1223.5	30.0	3927	2	US-08-996-644-1 Sequence 1, Appli
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39	1172	28.7	6143	1	US-08-612-521-3 Sequence 3, Appli
40	1116.5	27.4	3792	4	US-09-351-224E-10 Sequence 10, Appli
41	1116.5	27.4	3792	4	US-09-677-488A-10 Sequence 10, Appli
42	1116.5	27.4	3792	4	US-09-677-682B-10 Sequence 10, Appli
43	1032.5	25.3	3999	4	US-09-351-224E-9 Sequence 9, Appli
44	1032.5	25.3	3999	4	US-09-677-488A-9 Sequence 9, Appli
45	1032.5	25.3	3999	4	US-09-677-682B-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-023-655-1168
; Sequence 1168, Application US/09023655
; Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1168:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3924 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCES:
 ; LIBRARY: GENBANK
 ; CLONE: 5187501
 ; US-09-023-655-1168

Alignment Scores:

Pred. No.: 1,74e-291 Length: 3924
 Score: 2465.50 Matches: 478
 Percent Similarity: 76.46% Conservative: 149
 Best Local Similarity: 58.29% Mismatches: 182
 Query Match: 60.44% Indels: 11
 DB: 4 Gaps: 3

US-09-873-409-2 (1-812) x US-09-023-655-1168 (1-3924)

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 QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
 DB 1455 GTGAGTCAGAGCGCGTCTGTTTCCACCAATTCCTGAAATATTGTTATGGCGGT 1514
 QY 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
 DB 1515 GSAATGTAAACCATGATGAGATAGAAAGCTGTCAAAGAGGCGCAACGGCTATGAGTTT 1574
 QY 62 IleValGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
 DB 1575 ATCAAGAAATACCAAGAAATTTGACACCTGTTGGAGAGAGGCGCCACCTGAGT 1634
 QY 82 GlyGlyGlnLysGlnArgIleAlaAlaAlaArgAlaValArgAsnProLysIleLeu 101
 DB 1635 GGTGGGCGAAGACAGAGATGCCATTGCACGTCCTGTTGGAGAGAGGCGCCACCTGAGT 1694
 QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
 DB 1695 CTGCTGGATAGGCGCCAGCTGACATGACACAGAAAGTGAAGCTGAGGTACAGGCGCT 1754
 QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
 DB 1755 CTGGATAGGCGAGAGAGCGCGACCACTTGTGATAGCACACCGACTCTCTACGGTC 1814
 QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
 DB 1815 CGAAATGCAGATGTCATCGCTGGGTTTGAGGATGGAGTAATTTGGAGCAAGGAGCCNC 1874
 QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal----- 175
 DB 1875 AGCGAATCTGTAGAGAGAGGAGGCTGTACTTCAAACTTGTCAACATCGACATCAGGA 1934
 QY 176 -----MetSerGlnAspIleLysLysAlaAspGluGlnMetGluSerMetThrTyr 192
 DB 1935 AGCCAGATCCAGTCAGAGAAATTGAACTAATGATGAAAGGCTGCCACCTAGAAATGCC 1994
 QY 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
 DB 1995 CCAATGGCTGGAAATCTCGCCTATTAGGCATTTCTACTCAGAAATAAATCTTAAATTC 2054
 QY 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluIleSerLeuProGlu 230
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 QY 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluThrProPheValValLeuGly 250

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 DB 2475 ACAAGACTTGGCCACAGATGCTGCCAAGTCCCAAGGAGCCACAGAAACCGAGTTGGCTTTA 2534
 QY 371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleTyrGlyTyr 390
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 QY 411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHisAlaGlyLys 430
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 QY 551 ProAsnIleAspSerArgSerGlnGlyLysLysProAspThrCysGluGlyAsnLeu 570
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QY 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
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QY 771 AlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGlnGlnGly 790
DB 3735 ACCATCCAGATGCGAGCTTATAGTGTGTTTCAGATGCGAGAGTCAAGAGAGTGGC 3794
QY 791 ThrHisGlnGlnLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
DB 3795 AGCATCAGCAGCTGCTGACAGAAAGCAGCTATTTTCAATGCTCAGTGTCCAGCT 3854

RESULT 2

US-09-762-195-2
; Sequence 2, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Stremler, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT FILING DATE: US/09/762,195
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP99/02426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-2

Alignment Scores:
P-Id. No.: 1.74e-281 Length: 3924
Score: 2465.50 Matches: 478
Percent Similarity: 76.46% Conservative: 149
Best Local Similarity: 58.23% Mismatches: 182
Query Match: 60.44% Indels: 11
Gaps: 4

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QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1455 GTGAGTCAGAGCGCGTCTGTTTCCACCACCAATGCTGAAATATTTGTTATGGCCGT 1514
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DB 1515 GGAATGTAACCATGGATGAGATAAGAAAGCTCTCAAGAGGCCAACCCCTATGAGTTT 1574
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
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QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 1635 GGTGGGAGAGCAGAGGATCGCCATTCGACGTGCTGTTGTTCCACCCCAAGATCCTT 1694
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGlnSerLysSerAlaValGlnAlaAla 121
DB 1695 CTGCTGATGAGGCGCAGCTCAGCATTCGACACAGAAAGTGAAGCTGAGSTACAGCAGCT 1754
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
DB 1755 CTGATAGGCCAGAGAGGGCCGACCCCATTTGATAGCACCCGACTGTCTACGGTC 1814
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1815 CGAAATGCGATGTCATCGCTGGGTTTGGAGTGGAGTAAATTTGGAGCAAGGAAGCCAC 1874
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal 175
DB 1875 AGCGAATGATGAAGAAGAGGAGGCTGCTCTCAAACTTGTCAACATGCGACACATCAGGA 1934
QY 176 -----MetSerGlnAspIleLysAlaAspGluGlnMetGluSerMetThrTyr 192
DB 1935 AGCCAGATCCAGTCAGAAAGATTTGAATAATGATGAAAGGCTGCCACTAGAAATGCC 1994
QY 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
DB 1995 CCAATGGCTGGAATCTCGCTATTTAGGCATTTCTACTCAGAAAAACCTTTAAAAATTC 2054
QY 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluIleSerLeuProGlu 230
DB 2055 CAAATGTCAGAAAGACCTTGATGTGGAACCCGATGCGACTTGAAGCAATGTCACCA 2114
QY 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrPropheValValLeuGly 250
DB 2115 GTGTCTCTTCTGAAGTCTCTGAAACTGATAAAACAGATGGCCCTACTTTGTGTGGGA 2174
QY 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
DB 2175 ACATGATGCCATTTGCCAATGGGGGCTTCAGCGGCATTTTCAGTCATTTCTCAGAG 2234
QY 271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr 290
DB 2235 ATCATAGCGATTTTGGACCGGCGATGATGTCAGTGAAGCAGCAGAAAGTGCACATATTC 2294
QY 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
DB 2295 TCTTTGATTTCTTATTTCTGGGAATTTATTTCTTTTCTTTTCTTTCTTTCTTTCTTTCT 2354
QY 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
DB 2355 ACCTTTGGGAAAGCTGCGAGATCTCTCACCAGAGACTGCGGTCAATGGCTTTTAAAGCA 2414
QY 331 MetLeuTyrGlnAspIleAlaThrPheAspGluLysGlnAsnSerThrGlyLeuThr 350

2415	ATGCTAAGACAGGACATAGCTGGTGTGATGACCATAAACAGTACTGTGGTCACATTTCT	2477
Qy	351 ThrIleuEtaIleAspIleAlaGlnIleGlnIleValaThrGlySerArgIleGlyVal	370
Db	2475 ACAAGACTTGCACAGATGCTGCCAAGTCCAAGGAGCCACAGACCGATTTGGCTTTA	2534
Qy	371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleIleGlyTrp	390
Db	2535 ATTGCACAGATATAGCTAACCTTTGGACCTGGTATTATCATATCATTTATCTACGGTGG	2594
Qy	391 GluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGlyMetIleGlu	410
Db	2595 CAGTTAACCTATTGCTATTAGCAGTTGTTCCAAATTATGCTGTGTCAGGAATTGTGAA	2654
Qy	411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnIleuLysHisAlaGlyLys	430
Db	2655 ATGAATTTGTGGCTGGAATGCCAAAGAGATAAAAGAAGACTGGAAGCTGCTGGAAG	2714
Qy	431 IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla	450
Db	2715 ATTGCACAGAGCAATAGAAATATTATAGACAGTTGTGTCTTTGACCCAGGAAGAAA	2774
Qy	451 PheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla	470
Db	2775 TTTGAATCAATGTATGTTGAAAAATTGTATGGACCTTACAGGAATCTGTGCAGAAGCA	2834
Qy	471 GlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleIleTyrPheAlaTyrAla	490
Db	2835 CACATCATGGAATTACTTTTAGTATCTCACAGCATTTATGATTTTTCCTATGCCGT	2894
Qy	491 GlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPhe	510
Db	2895 TGTTTTCGATTTGGTGCAATATCTCATTTGTAATGCATATGCGCTTCAGAGATGTTATT	2954
Qy	511 IleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValLeuAla	530
Db	2955 CTGGTGTTTCTGCAATGTATTGTGGTCAGTGGCTCTAGGACATGCCAGTTCAATTGCT	3014
Qy	531 ProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuGluLysLys	550
Db	3015 CCAGACTATGCTAAAGCTAGCTGCTCGAGGCCACTATTATCATGCTGTTTGAAGACAA	3074
Qy	551 ProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGluGlyAsnLeu	570
Db	3075 CCTCTGATTACACAGCTACAGTGAAGAGGGGCTGAAGCCTGATAAATTTGAAGGAATATA	3134
Qy	571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly	590
Db	3135 ACATTTAATGAATGCTGTTCAACTATCCACCCGACCAACGTGCCAGTGTTCAGGG	3194
Qy	591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly	610
Db	3195 CTGAGCTCGAGGTGAAGAAAGGCCACAGACTAGCCCTGGTGGGCAGCAGTGGCTGGGG	3254
Qy	611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu	630
Db	3255 AAGAGCAGGTGTTCAGCTCTCTGGAGCGGTCTTACAGCCCTTTGGCGGGGACAGTGTCT	3314
Qy	631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGlnIleAlaIle	650
Db	3315 CTCGATGTCAAGAAGCAAGAAACTCAATGTCTCAGTGGCTCAGAGCTCAACTCGGAATC	3374
Qy	651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp	670
Db	3375 GTGTCTCAGAGCCTATCTCTATTATTGACTGCAGCAATGCCAGAAATATTCCTATGAGAC	3434
Qy	671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis	690
Db	3435 AACAGCCGGTGTGTATCACAGGATGAATTTGTAGTGCAGCCAAAGCTGCCACATCAT	3494
Qy	691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln	710
Db	3495 CCTTTCTACAGACGTTTACCCCACAATATGAACACAGATGGGAGATAGGGGACTCAG	3554

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Qy 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
Db 3555 CTCCTCAGGAGGTCAAAAACAGAGGATTGCTATTGCCGAGCCCTCATACAGACACCTCAA 3614
Qy 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGlnLysValValGln 750
Db 3615 ATCCTCTGTTGGATTGAGCTACATCAGCTCTGGTGAAGAGTGAAGAGGTGTGTCCAA 3674
Qy 751 HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer 770
Db 3675 GAAGCCCTGGCAAAAGCCAGAGAACGCCGACCTGATTGTGTGATGCTCACCCCTGTGTC 3734
Qy 771 AlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGlnGlnGly 790
Db 3735 ACCATCCGAATCCAGACTTAATAGTGTGTTCAGATGGGAGAGTCAAGGAGCATGGC 3794
Qy 791 ThrHisGlnGlnLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
Db 3795 ACGCATCAGCAGCTGTCTGGCACAGAAAGGCATCTATTTTCAATGGTCAAGTGTCCAGGCT 3854

RESULT 3
US-09-672-810-1
; Sequence 1: Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4186
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(3940)
US-09-672-810-1

Alignment Scores:
Pred. No.: 1,538-278 Length: 4186
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best Local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 4 Gaps: 5

US-09-873-409-2 (1-812) x US-09-672-810-1 (1-4186)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1456 GTTGATGGACAGATATTAGGACCAATAACGTAAAGGTCTACGGGAATCATCGGTGTG 1515
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1516 GTGAGTCAGGAACCTGTATTGTTTGGCCACCATAGCTGAAACCAATTCCTATGTCGT 1575
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1576 GAAGATGTCACCATGGATTGAGAAAGCTGTCAGGAAGCCATGCGCTATGACTTT 1635
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGlnLysGlyAlaGlnMetSer 81
Db 1636 ATCATGAACCTGCTCAGAAATTTCACCCCTGGTTGGAGAGAGAGGGGCCACGCTGAGT 1695

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Db 3850 GTCAGGAGCGGACACATCAGCAGCTGCTGGCAGAAAGGACCATATTTTCAATG 3909
Qy 806 ValAsnAlaGlnSer 810
Db 3910 GTCAGTGTCAGGCT 3924

RESULT 4
US-09-672-810-3
; Sequence 3, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STRIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4195
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(3949)
US-09-672-810-3

Alignment Scores:
Pred. No.: 1,58e-278 Length: 4195
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 4 Gaps: 5

US-09-873-409-2 (1-812) x US-09-672-810-3 (1-4195)
Qy 2 ValAspGluAsnAspIleAraAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1465 GTTGATGGACAGGATATTAGGACCAATTAACGTAAGGTTTCTACGGGAAATCATCGGTGTG 1524
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1525 GTGAGTCAGGAACCTGTATTTGTTTCCACCCAGATAGCTGAAACATTCGCTATGTCGT 1584
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1585 GAAGATGTCACCATGGATGAGATTGAGAAAGCTGTCAAGGAAGCCCAATGCTATGACTTT 1644
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1645 ATCATGAAGTCCTCTGAAATTTTGACACCTCGTGTGGAGAGAGGGGCCAGCTGAGT 1704
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1705 GGTGGCAGAGAGCAGAGGATCGCAATTCGCTGCCCTGCTGGTTCGCAACCCCAAGATCCTC 1764
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1765 CTGCTGGACGAGGCGACGCTGAGCTTGGACACAGAAAGTGAAGCAGGTGGTTCAGGTGGCT 1824
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 1825 CTGGATAGGCCAGAAAGGTGGACCAACCATTTGTGATAGCTCATCGTTTGTCTACGGTT 1884
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
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Db 1885 CGTAATGCCAGCGCTCATCGCTGTTTCGATGATGGAGTCATTGTGGAGAAAGGAATCAT 1944
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle 180
Db 1945 GATGAGCTCATGAAGAGAAAGGCACTTACTTCAAACTTGTCAAAATGTCAGACAGCAGGA 2004
Qy 181 -----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191
Db 2005 AATGAAATTTGAATTAGAAATGAGCTGATGATTCAAAAGTGAAATTTGATACCTTTGGAA 2064
Qy 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206
Db 2065 ATGCTCTTCATCATCAATTCAGATCCAGCTCTAATAAGAAAGATCCACTCGTAGGAGTGC 2124
Qy 207 LysSerIleLysSerAspPheIleAspLysAlaGluGluSerThrClnSerLysGluIle 226
Db 2125 CGTGGATCAAGGCCAA-----GACAGAAAGCTTTAGTACCAAGAGAGCTCTGGATGAA 2178
Qy 227 SerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrProPhe 246
Db 2179 AGTATACCTCCAGTTTCTTTTGGAGGATTATCAAGCTAAATTTAACTGAGTGGCCTTAT 2238
Qy 247 ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle 266
Db 2239 TTTGTTTGGTGTATTTTGTGCCATTATAAATGGAGGTCTGCAACACAGCAATTTGCAGTA 2298
Qy 267 IlePheAlaLysIleIleThrMetPhe---GlyAsnAsnAspLysThrThrLeuLysHis 285
Db 2299 ATATTTTCAAGATTATAGGATTTTACAGAAATGATGATGCCCAACAAACACGACAG 2358
Qy 286 AspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr 305
Db 2359 AATAGTAACCTGTTTCTACTATTGTTTCTAGTCTTGGAAATTTGTTTCTTTTATTACATT 2418
Qy 306 PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis 325
Db 2419 TTCCTTCAGGCTTCACTTTCGAAAGCTGAGAGATCCTCACCAGGCGCTCCGATAC 2478
Qy 326 LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSer 345
Db 2479 ATGGTTTTCGATCCATGCTCAGACAGGATGTGAGCTGTTGATGACCTAAAAACACC 2538
Qy 346 ThrGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
Db 2539 ACTGGAGCAATTGACTACCGAGCTCGCAATGATGCTGCTCAAGTTAAAGGGGCTATAGT 2598
Qy 366 SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleSer 385
Db 2599 TCCAGGCTTGTATATATTACCCAGATATAGCAAAATCTTGGCAGACAGGAATAATTATCC 2658
Qy 386 PheIleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
Db 2659 TTAATCTATGGTGGCAACTGACACTGTTACTCTTAGCAATTTGTACCCCATCATTTGCAATA 2718
Qy 406 ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
Db 2719 GCAGGAGTTTGTGAATGAATGTTGTCTGGCAGACGACTGAAGATGAAGAAAGAACTA 2778
Qy 426 LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445
Db 2779 GAAGTGTCTGGGAAGATCGCTACTGAAGCAATAGAAAACCTCCGAACCTGTTGTTCTTG 2838
Qy 446 ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465
Db 2839 ACTCAGACAGAGAGTTTGAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 2898
Qy 466 ThrSerLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr 485
Db 2899 TCTTTGAGGAAAGCACACACTCTTTGGAATCAAGCTTTTCCCTTCACGAGGCAATGATGAT 2958
Qy 486 PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr 505
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; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT APPLICATION NUMBER: US/09/762,195
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP99?02426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1

Alignment Scores:
Pred. No.: 5,67e-278 Length: 3988
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: Gaps: 4

US-09-873-409-2 (1-812) x US-09-762-195-1 (1-3988)
QY 2 ValAspGluuAsnAspIleArgAlaLeuAenVala:GHISrTyArgAspHisIleGlyVal 21
Db 1423 GTTGTGACAGACGATATTAGGACCAATAATGTAAGGTTTCTACGGGAAATCATTTGCTGTG 1482
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleIysrTyGlyArg 41
Db 1483 GTGAGTCAGAAACCTGTATTGTTTCCACCAGATAGCTGAAAAACATTCGCTATGCGCGT 1542
QY 42 AspAspValThrAspGluMetGluArgAlaAlaAArgGluAlaAsnAlaTyRAspPhe 61
Db 1543 GAAATATGTCACCATGATGAGATTGAGAAAGCTGTCAAGGAAGCCAATGCCTATGACTTT 1602
QY 62 IleMetGluPheProAsnIysPheAsnThrLeuValGlyGluIysGlyAlaGlnMetSer 81
Db 1603 ATCATGAAGAACTGCCCTCATAAATTTGACACCTTGTTGGAGAGAGAGGGCCCGATGAGT 1662
QY 82 GlyGlyGlnIysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProIysIleLeu 101
Db 1663 GGTGGGCGAAGACAGAGGATGCCATTGACGTGCGCTGGTTTCGCAACCCCAAGATCCCTC 1722
QY 102 IleLeuAspGluAlaThrSerIleLeuAspSerGluSerIysSerAlaValGlnAlaAla 121
Db 1723 CTGCTGAGATGAGCGCACGCTGACCCCTTGGACAGAGAAGCGAAGCATGGTTCAAGTGGCT 1782
QY 122 LeuGluIysAlaSerIysGlyArgThrThrIleValAlaAlaHisArgLeuSerThrIle 141
Db 1783 CTGGATAGGCCAGAAAGCTCGACCCATTGTGATAGCTCATCGTTTGTCTACAGTT 1842
QY 142 ArgSerAlaAspLeuIleValThrLeuIysAspGlyMetLeuAlaGluIysGlyAlaHis 161
Db 1843 CGTAATGCTGACGTCATCGCTGTTTCGATGATGCGAGTCATTGTGAGAGAAGCAAAATCAT 1902
QY 162 AlaGluLeuMetAlaIysArgGlyLeuTyTySerLeuValMetSerGln----- 178
Db 1903 GATGAACCTCTGAAGAGAAAGGCATTACTTCAAACTGTGCATATGCAGACAGCAGGA 1962
QY 179 -----AspIleIysLysAlaAspGluGlnMetGluSerMetThrTySerThrGlu 195
Db 1963 AATGAAGTTGAATTAGAAAAATGACGTGATGAATCCAAAGATGAAATTCATGCGCTGGAA 2022
QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 2023 ATGCTCTCAATGATTCAAGATCCAGTCTTAATAGAAAAAGATCAATCGTAGGAGTGTCT 2082
QY 210 Lys---SerAspPheIleAspIysAlaGluGluSerThrGlnSerLysGluIleSerLeu 228

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Db 2083 CGTGATCAAGCCCAAGACAGAAAGCTTAGTACCAAGAGAGGCTCTGGATGAAGATATA 2142
Qy 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluIuPProPheValVal 248
Db 2143 CCTCCAGTTTCCTTTGGAGGATATGAAGCTAAATTAACCTGAATGCCCTATTATTTGT 2202
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2203 GTTGGTGTAATTTGTGCAATTAATAAGCGAGCTGCAACAGCAGATTTGCAATATATTT 2262
Qy 269 AlaLysIleLeuThrMetPheGlyAsn--AsnAspLysThrThrLeuLysHisAspAla 287
Db 2263 TCAAGATTATAGGGTTTTCACAGAAATTCATGATCTCTGAAACAAAGCAGCAATAGT 2322
Qy 288 GluIleThrSerMetIlePheValIleLeuGlyValIleCysPheValSerThrPheMet 307
Db 2323 AACTGTGTTTCTACATTTCTAGCCCTTGAATTAATTTCTTTTATTAATTTTCTT 2382
Qy 308 GlnGlyLeuPheThrGlyArgAlaGlyIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2383 CAGGGTTTCACATTTGGCAAGCTGGAGAGATCTCACCAAGCGGCTCCGATACATGTT 2442
Qy 328 PheLysAlaMetLeuThrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
Db 2443 TTCCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGTATGACCCCTAAACACCACTGGA 2502
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 2503 GCATTTGACTACAGCTCCCAATGATGCTCTCAAGTTAAGGGCTATAGGTTCCAGG 2562
Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2563 CTTCGTGTAATACCCAGAAATATAGCAAACTCTGGACAGGATAATATATATCTCTCATC 2622
Qy 388 TyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2623 TATGTTGGCACTAACACTGTTACTCTTACGAATTTGACCAATTTGACCAATTTGACAGGA 2682
Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLysHis 427
Db 2683 GTTGTGTAATGAAATCTTGCTGGCAAGCACTGAAAGATAAGAAAGAACTAGAAAGT 2742
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 2743 GCTGGGAAGATCGCTACTGAAGCAATAGAAACCTCCGAAACCTGTTCTTTCCTTACACTAG 2802
Qy 448 GluLysAlaPheGluGlnMetThrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 2803 GAGCAGAGTTGAACATATGTTGCTCAGAGTTGAGGTACCATACAGAACTCTTTG 2862
Qy 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleThrPheAla 487
Db 2863 AGGAAGCACACATCTTTGGAATTACATTTCTTCCCTCACCCAGGCAATGATGATTTTCC 2922
Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaThrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 2923 TATGCTGATGTTTCCGTTTGGAGCTTACTTGTGGCCACATAAATCATGAGCTTTGAG 2982
Qy 508 GlyMetPheIleValPheThrAlaIleAlaThrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 2983 GATGTTCTGTAGTATTTTCACTGTTCTTGTGTCATGGCCATGGCCGTGGGCAAGTCAGT 3042
Qy 528 ValLeuAlaProGluThrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3043 TCAITTTGCTCTGATGTCGCAAGGCCAAATATACAGCAGCCCATCATCATCATCAT 3102
Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3103 GAAGAAACCCCTTTGATTTGACAGCTTACAGCAGGAGGCCCTAATAGCCGACACATTTGAA 3162
Qy 568 GlyAsnLeuGluPheArgGluValSerPheThrThrProCysArgProAspValPheIle 587

Db 3163 GGAATGTCACTTTGGTGAAGTTGTTATTAACATATCCACCCGACCGACATCCCAAGT 3222
Qy 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3223 CTTTCCAGGACTGAGCTCGAGGTTGAAGAGGGCGACAGCTGCTCTGGTGGCGCAGCAGT 3282
Qy 608 GlyCysGlySerThrSerValGlnIleLeuGlnArgLeuThrAspProValGlnGly 627
Db 3283 GGTCTGGGAAGACACAGCTGTTCCAGCTCTCTGGAGCGGTTCTACGACCCCTTGGCAGGG 3342
Qy 628 GlnValLeuPheAspGlyValAlaLysGluIleAsnValGlnTrpLeuArgSerGln 647
Db 3343 AAGTGTCTGCTTATGATGCAAGAAATAAAGCGACTCAATGTTTCACTGGCTCCGAGCACAC 3402
Qy 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3403 CTGGGATGTTGTCAGGAGGCCATCTCTGTTGACTGACGATTTCTGAGAACTTGC 3462
Qy 668 TyrGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsnAlaAla 687
Db 3463 TATGGAGACACAGCGCGGTGTTGTTCACAGGAAGAGATTGTGAGGGCAGCAAGAGGCGC 3522
Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysThrAsnThrGlnValGlyLeuLys 707
Db 3523 AACATACATGCTTCTATCGAGTCACCTGCTTAATAATATAGCACTAAGTAGGAGACAAA 3582
Qy 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3583 GGAACCTCAGCTCTCTGGTGGCCAGAAACCAACGATTCATGCTGCTGCTTGTAGA 3642
Qy 728 LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 3643 CAGCCTCATATTTTGTGTTTGGATGAAGCCACGCTCAGCTCTGGATACAGAAAGTGAAG 3702
Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3703 GTTGTCCAGAGCCCTGCAAGCAAGCCAGAGAGCCGACCTGCTGATTTGATTCAC 3762
Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 3763 CGCCTGTCCACCATCCAGATGAGCACTTAATAGTGTGTTTTCAGAAATGCGCAGAGTCAAG 3822
Qy 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleThrPheLysLeuValAsn 807
Db 3823 GAGCATGGCAGCGATCAGCAGCTGCTGGCAGAAAGGCACTATTTTTCAATGTCAGT 3882
Qy 808 AlaGlnSer 810
Db 3883 GTCCAGGCT 3891

RESULT 6
US-08-784-649A-1
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sikic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/784,649A		210 lys---SerAspPheIleAspIleAlaGluGluSerThrGlnSerIleGluIleSerIleu 228	
FILING DATE:		2155 CQTGGATCACAAGCCCAAGACGAGCTAGTACCAAGAGGCTCTGGATGAAAGTATA 2214	
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: Sherwood, Pamela J			
REGISTRATION NUMBER: Reg No. 5830697 36,677			
REFERENCE/DOCKET NUMBER: 06037/007001			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 415-322-5070			
TELEFAX: 415-854-0875			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 4264 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA			
US-08-784-649A-1			
Alignment Scores:			
Pred. No.:	6,39e-278	Length:	4264
Score:	2436.00	Matches:	466
Percent Similarity:	76.79%	Conservative:	166
Best Local Similarity:	56.62%	Mismatches:	177
Query Match:	59.72%	Indels:	14
DB:	2	Gaps:	4
US-09-873-409-2 (1-812) x US-08-784-649A-1 (1-4264)			
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Db	1495	GTTGATGGCAGCAGGATATTAGGACCAATAATTAAGGTTTCTACGGGAATCATTCGTGTG 1554	
Qy	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnIleIleIleIleIleIleIle 41	
Db	1555	GTGAGTCAGGAACCTGATTTGTTCCACCCAGATAGCTGTCAAGAAACATTCGCTATGCGCT 1614	
Qy	42	AspAspValThrAspGluMetGluArgAlaAlaAlaArgGluAlaAsnAlaTyrAspPhe 61	
Db	1615	GAAATGTCACCATGATGAGATGAGAAAGCTGTCAAGGAAGCCAAATGCTATGACITP 1674	
Qy	62	IleMetGluPheProAsnIlePheAsnThrLeuValGlyGluIleGlyAlaGlnMetSer 81	
Db	1675	ATCATGAATGCTCATAAATTTGACACCTGTTGGAGAGAGAGGGCCGAGTGTGAGT 1734	
Qy	82	GlyGlyGlnArgIleAlaIleAlaAlaAlaLeuValArgAsnProIleIleIleIleIle 101	
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Qy	102	IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerIleSerAlaValGlnAlaAla 121	
Db	1795	CTGCTGGATGAGCCACGTCAGCTTGGACACAGAAAGCGAGCGAGTGTGAGTGTGCT 1854	
Qy	122	LeuGluIleAlaSerIleValThrIleValValAlaAlaHisArgLeuSerThrIle 141	
Db	1855	CTGGATAGCCAGAAAGGTGGACCCATTTGTGATGCTCCTGTTTGTCTACAGTT 1914	
Qy	142	ArgSerAlaAspLeuIleValThrLeuIleAspGlyMetLeuAlaGluIleGlyAlaHis 161	
Db	1915	CGTAATGCTGACGTCATGCTGTTTCGATGATGAGTCAATTCGAGAGAAAGAAATCAT 1974	
Qy	162	AlaGluLeuMetAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 178	
Db	1975	GATGAACCTATGAAGAGAGAGGCAATTTACTTCAAACTGTGTCACATGCGACACAGCA 2034	
Qy	179	-----AspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 195	
Db	2035	AATGAAGTTGAATTAGAAATGACGCTGATGATCCAAAGTGAATGATTCCTTGGAA 2094	
Qy	196	ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209	
Db	2095	ATGCTCTCAATGATTCAAGATCCAGCTAATAAGAAAGAAAGATCACTCGTAGGAGTGTG 2154	
Qy	568	GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587	
Db	3115	TCATTTGCTCTGACTATGCCAAAGCAAAATATATCAGCAGGCCCATCATCATGATCAT 3174	
Qy	548	GluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 567	
Db	3175	GAAAAAACCCCTTTGATGTGACGCTACAGCAGGAAGGCTTAATGCGCAACACATTTGAA 3234	
Qy	528	ValLeuAlaProGluTyrSerIleAlaIleIleIleIleIleIleIleIleIleIleIle 547	
Db	3115	TCATTTGCTCTGACTATGCCAAAGCAAAATATATCAGCAGGCCCATCATCATGATCAT 3174	
Qy	508	GlyMetPheIleValPheThrAlaIleAlaIleAlaIleAlaIleGlyIleThrLeu 527	
Db	3055	GATGTCGTGTGATTTTTCAGCTGTTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3114	
Qy	528	ValLeuAlaProGluTyrSerIleAlaIleIleIleIleIleIleIleIleIleIleIle 547	
Db	3115	TCATTTGCTCTGACTATGCCAAAGCAAAATATATCAGCAGGCCCATCATCATGATCAT 3174	
Qy	548	GluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 567	
Db	3175	GAAAAAACCCCTTTGATGTGACGCTACAGCAGGAAGGCTTAATGCGCAACACATTTGAA 3234	
Qy	568	GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587	

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Db 3235 GGAATGTCACATTTGGTGAAGTGTATTCACATATCCACCGACCGACATCCAGTG 3294
Qy LeuArgGlyLeuSerLeuSerLeuGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3295 CTTGAGGAGTGAAGTGGAGTGAAGAGGCGCAGAGCTGCTCTGGTGGCAGCAGT 3354
Qy GlyCysGlyLysSerThrSerValGlnLeuGlnArgLeuLysProValGlnGly 627
Db 3355 GCGTGTGGAGAGCAGCAGTGGTCCAGCTCTCGAGCGGTCTACAGCCCTTGGCAGGG 3414
Qy GlnValLeuPheAspGlyValAlaPheAlaLysGluLeuAsnValGlnTrpLeuArgSerGln 647
Db 3415 AAAGTGTCTGTGATGCAAGAAATAAAGCGACTGAATGTTTCAGTGGCTCCGAGCAC 3474
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Db 3475 CTGGGCACTGTGTCAGAGAGCCCTCTGTTGACTGCGAGCTTGTCTGAGAACATTGCC 3534
Qy TyrGlyAspAsnSerArgValValProLeuAspGluLysGluAlaAlaAsnAlaAla 687
Db 3535 FATGGAGACAACAGCGGTGGTGTCTACAGAGAGATTGTGAGGGCGCAAGAGGAGGCC 3594
Qy AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
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Qy GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3655 GGAATCAGCTCTCTGTGGCCAGAAACAAGCATGTCCTGCTGCTTGTAGA 3714
Qy LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 3715 CAGCTCATATTTTGGTGTGGATGAGAGCCAGCTGCTGATGATGATGATGATGATG 3774
Qy ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
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Qy ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 3835 CGCTGTGCCACATCCAGATGCAAGTCTTAATAGTGGTGTTCAGATGCGAGATGCAAG 3894
Qy GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleFyrPheLysLeuValAsn 807
Db 3895 GAGCATGGCAGCATCAGCAGTCTGTCGACAGAAAGGCATCTATTTTCAATGGTCAGT 3954
Qy AlaGlnSer 810
Db 3955 GTCCAGGCT 3963

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RESULT 7

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US-08-784-649A-5
; Sequence 5, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Chen, Gang
; APPLICANT: Siki, Branimir I
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-5

Alignment Scores:
Pred. No.: 6,396-278 Length: 4264
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 2 Gaps: 4

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US-09-873-409-2 (1-812) x US-08-784-649A-5 (1-4264)

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Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1555 GTGAGTCAGAACCTGTATTGTTTCCACCATAGCTAGCTGAAACATTCGCTATGGCCGT 1614
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1615 GAAATGTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
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Db 1735 GTTGGGCAAGACAGAGGATCGCCATTCACGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1794
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1795 CTGCTGGATGAGCCCGCCAGTCAGCTTGGACAGAAAGCGAGCAGTGGTTCAGGTGGCT 1854
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 1855 CTGGATAAGCCAGAAAGGTCGACCATTTGATAGTACCTCATCGTTTGTCTACAGTT 1914
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGlyLysGlyAlaHis 161
Db 1915 CGTAATGCTGACGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1974
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln----- 178
Db 1975 GATGAACCTCATGAAAGAGAGAGCATTTACTTCAAACTTGTTCACATGTCAGACAGAGA 2034
Qy 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
Db 2035 ATGAAGTTGAATAGAAATGACGCTGATGATGATGATGATGATGATGATGATGATGATG 2094
Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 2095 ATGCTCTCAATGATTCAGATCCAGTCTAATAAGAAAGAAAGTCAACTCGTAGGAGTGTC 2154

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QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
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QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyThrValAlaPheValIleGlySerSer 607
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QY 608 GlyCysGlyLeuSerThrSerValGlnLeuGlnArgLeuTyrAspProValGlnGly 627
Db 3355 GCGTGTGGGAAGACACAGTGTCTGAGTCTCTGAGCGGTCTTACGACCCCTTGGCAGG 3414
QY 628 GlnValLeuPheAspGlyValAlaGlyGluLeuAsnValGlnTyrLeuArgSerGln 647
Db 3415 AAAGTCTGCTGTGATGGCAAGAAATAAAGGACTGTAATGTTCTGATGGCTCCGAGCAC 3474
QY 668 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3475 CTGGCATCGTGTCCAGAGCCCATCTGTGTGACTGCAGCATTCGTGAGACATTCGCC 3534
QY 668 TyrGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsnAlaAla 687
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QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 3595 AACATACATGCTTTCATCGAGTCACTGCTTAATAATATAGCATTAAGTAGGAGACAAA 3654
QY 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
Db 3655 GGAAGTCTCTGCTGGCCAGACACAGCATTCGCATAGCTCGTCCCTTGTGAGA 3714
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnSerGluLys 747
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QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3775 GTTGTCCAGAGCCCTGGACAAAGCCAGAGAGCCGACCTGCATTTGTGATTTGCTCAG 3834
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 3835 CGCTGTCCACCATCCAGATCCAGACTTAATAGTGGTGTTCAGAAATGGCAGAGTCAAG 3894
QY 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
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QY 808 AlaGlnSer 810
Db 3955 GTCCAGGCT 3963
RESULT 8
US-08-181-471-2
; Sequence 2, Application US/08181471
; Patent No. 5641508
; GENERAL INFORMATION:
; APPLICANT: Li, Lingna
; APPELLANT: Lishko, Valeryi K.
; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
; COMPOSITIONS TO HAIR FOLLICLES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Pitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

QY 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 226
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QY 229 ProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248
Db 2215 CTTGAGTCTCTTTTGGAGGATTATGAAGCTAAATTTAACTCAATGGCTTATTTGT 2274
QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2275 GTTGGTGTATTTTGGCCATTATAAGAGGCTGCAACAGCATTTGCAATAATATT 2334
QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
Db 2335 TCAAGATTATAGGGGTTTTCACAGATTGATGATCTCTGAAACAAACAGCAGAGTAT 2394
QY 288 GluIleTyrSerMetIlePheValIleGluValIleCysPheValSerTyrPheMet 307
Db 2395 AACTGTTTCTACTATTGTTCTAGCCCTTGAATTAATTTCTTATTACATTTTCTT 2454
QY 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluLeuLeuThrMetArgLeuArgHisLeuAla 327
Db 2455 CAGGGTTTCACATTGGCAAGCTGGAGAGATCTCCACAGGGCTCGATACATGTT 2514
QY 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
Db 2515 TTCCGATCCATGCTCAGACAGGATGTGAGTGTGTTGATGACCCCTAAACACACCAGTGA 2574
QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
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QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2635 CTTGCTGTAATACCCAGAAATATAGCAATCTTGGACAGGAATAATATATCTTCTATC 2694
QY 388 TyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2695 TATGGTGGCAACTAACCTGTTACTCTTAGCAATGTACCCATCATTTGCAATAGCAGA 2754
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
Db 2755 GTTGTGTAATGAATGTTGCTGGACAGCACTGAAAGATAAGAAAGACTAGAGT 2814
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 2815 GCTGGAGATCGCTACTGAGCAATAGAAACTTCCGAAACCGTTGTTCTTTGACTCAG 2874
QY 448 GlyLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
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QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
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QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3055 GATGTTCTCTAGTATTTTCACTGTGTCTTTGTTGCTGCTGCTGCTGCTGCTGCTGCT 3114
QY 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3115 TCATTGCTCTGACTATGCCAAAGCCAAATATATCAGCAGCCCATCATCATCATCATCAT 3174
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLeuLysProAspThrCysGlu 567
Db 3175 GAAAAACCCCTTTGATTGACAGCTACAGCAGGAGGCTTAATGCTCCAAACATTTGAA 3234

CURRENT APPLICATION DATA: US/08/181.471
 APPLICATION NUMBER: 424
 FILING DATE: 13-JAN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,553
 FILING DATE: 02-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pittling, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: ANT0029P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 425..4267
 US-08-181-471-2

Alignment Scores:
 Pred. No.: 7,438-278 Length: 4646
 Score: 2436.00 Matches: 466
 Percent Similarity: 76.79% Conservative: 166
 Best Local Similarity: 56.62% Mismatches: 177
 Query Match: 14 Indels: 14
 DB: 4 Gaps: 4

US-09-873-409-2 (1-812) x US-08-181-471-2 (1-4646)

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 QY 22 ValSerGlnGluProValLeuPheGlyThrIleSerAsnAspIleGlyValArg 41
 DB 1841 GTGAGTCAGAACCTGTATTGTTCCACACAGATAGCTGAAACATTCGCTATGGCGGT 1900
 QY 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
 DB 1901 GAAATGTCCACATGATGAGTGTGAGAAAGCTGTCAAGGAAGCCAAATGCTATGACTTT 1960
 QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
 DB 1961 ATCATGAACCTCCATCAATTTGACACCTTGGTTGGAGAGAGGGGCCAGTTGAGT 2020
 QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
 DB 2021 GGTGGGACAGACAGAGGATGCCATTCAGTGCCTGCTGTGCAACCCCAAGATCCTC 2080
 QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
 DB 2081 CTGCTGGATGAGCCACGTCAGCTTGGACACAGAAAGCAGAGTGGTTCAGTGGCT 2140
 QY 122 LeuGluLysAlaSerLysGlyArgThrIleValValAlaHisArgLeuSerThrIle 141
 DB 2141 CTGGATAAGCCAGAAAAGTCCGACCAACCATTTGTGATAGCTCATCTGTTGTCTACAGTT 2200
 QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
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 QY 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
 DB 2321 AATGAAGTTGAATTAGAAATGAGCTGATGAATCCAAAGTGAAATGATGCTTGGAA 2380
 QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
 DB 2381 ATGCTCTCAATGATTCAAGATCCAGCTTAATAAGAAAAAGATCAACTCGTAGAGTGT 2440
 QY 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 228
 DB 2441 CGTGATCACAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCTCTGATGAAGATATA 2500
 QY 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValVal 248
 DB 2501 CCTCCAGTTTCCTTTTGGAGGATTATGAAGCTAAATTTAACTGAATGGCTTATTTGTT 2560
 QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
 DB 2561 GTTGGTGTATTTTGTGCCATTATAAATGGAGGCTGCAACCACTTTGCAATAATATT 2620
 QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
 DB 2621 TCAAGATTATAGGGCTTTTACAGAAATGATGATCCTGAAACAAACAGACAGATAGT 2680
 QY 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
 DB 2681 AACTGTGTTTCACTATTGTTTCTAGCCCTTGGAAATATTCTTTTATTATCATTTTCCCT 2740
 QY 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
 DB 2741 CAGGTTTCATTTGGCAAGCTGGAGAGATCTCACCAGCGGCTCCGATACATGGTT 2800
 QY 328 PheLysAlaMetLeuTyrGlnAspIleAlaTTPheAspGluLysGluAsnSerThrGly 347
 DB 2801 TTCGATCCATGCTCAGACAGGATGTGAGTTGTTGATGACCCCTAAACACACCTGGA 2860
 QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
 DB 2861 GCATTGCTACAGGCTCCGCAATGATGCTGCTCAGTTAAAGGGCTATAGTTCAGG 2920
 QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
 DB 2921 CTTGCTGTAATACCCAGAAATATAGCAAAATCTTGGGACAGAAATAATATATCTTCATC 2980
 QY 388 TyrGlyTTPGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
 DB 2981 TAGGTTGGCACTTAACACTGTTTACTCTTTCAGCAATGTCCCATCATTCGATGACGGA 3040
 QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLysHis 427
 DB 3041 GTTGTGAATGAAATGTTGTTCTGGACAGCACTGAAGATAGAAGAAAGACTAGAAGGT 3100
 QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerIleThrArg 447
 DB 3101 GCTGGGAAGATCGCTACTGAAGCAATAGAAATCTCCGAACCGTTGTTCTTTGACTCAG 3160
 QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
 DB 3161 GAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATCAGAAACTCTTTG 3220
 QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
 DB 3221 AGGAAAGCACACATCTTTGGATTTACATTTCTCCACCCAGCAATGATGATTTTTC 3280
 QY 488 TyrAlaAlaGlyPheArgPheGlyValThrLeuIleGlnAlaGlyArgMetThrProGlu 507
 DB 3281 TATGCTGAGTTTCCGTTTGGAGCTACTTGGTGCCACATAAATCATGAGCTTTGAG 3340
 QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
 DB 3341 GATGTTCTGTAGTATTTCAGCTGTTGCTTTGGTGCCATGCGCTGGGCGCAAGTCAGT 3400

QY 528 ValLeuAlaProGluTyrSerIysAlaIysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
DB 3401 TCATTGTCTCTGACTATGCCAAAGCAAAATATCAGCAGCCACATCATCATGATCAT 3460
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
DB 3461 GAAAAACCCCTTGTATGACAGCTACACAGCGAGGCTATGCCGACACATGGA 3520
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPhe 587
DB 3521 CGAAATGTCCATTTGGTGAAGTTGATTCAACTATCCACCCGACCGGACATCCAGG 3580
QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySer 607
DB 3581 CTTCAGGAGTGGCTTGGAGTGAAGAGGCGCAGACCTGCTCTGTGGGACAGT 3640
QY 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
DB 3641 GGCTGTGGAGAGACACAGTGTGTCAGCTCTGTGAGCGGTTCATGACCCCTTGGCAGG 3700
QY 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArgSerGln 547
DB 3701 AAAGTCTCTGTATGCGCAAGAAATPAAAGCGACTGAATGTCAGTGGCTCCGAGCAC 3760
QY 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
DB 3761 CTGGGCTATGTCCTCCAGGAGCCATCTCTGTGACTGCGAGCATTCCTGAGAACATTGCC 3820
QY 668 TyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaHisAlaAla 687
DB 3821 TATGGAGACAACACCGCGGTGTGTACAGAGAGAGATCGTCAGGCGCAGCAAGAGGCGC 3880
QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
DB 3881 AACATACATCCCTTCATCGAGTCACCTGCTTAATATATAGCACTAAAGTAGGAGCAAA 3940
QY 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
DB 3941 GGAACCTCAGCTCTCTGTGGCCAGAAACAGCATTCGCCATAGCTGTCCTTGTGATG 4000
QY 728 LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGlyLys 747
DB 4001 CAGCCTCATATTTGCTTTTGGATGAAGCCACGCTGCTGATACAGAAAGTGAAG 4060
QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
DB 4061 GTTGTCCAGAGCCCTGGACAGAGCCAGAGAGCGCGACCTGCATTCGATGCTCAC 4120
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
DB 4121 CGCCTGTCCACCATCCAGATGCGAGACTTAATAGTGTGTTTCAGATGSCAGAGTCAAG 4180
QY 788 GlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
DB 4181 GAGCATGCGACGATCAGCAGCTGCTGGCAGAAAGGCGATCTATTTTCATGCTCAGT 4240
QY 808 AlaGlnSer 810
DB 4241 GTCCAGGCT 4249

RESULT 9
US-09-023-655-1167
; Sequence 1167, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Alignment Scores:
Pred. No.: 7,436-278 Length: 4646
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 4 Gaps: 4
US-09-873-409-2 (1-812) x US-09-023-655-1167 (1-4646)
QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1781 GTTGATGGACAGGATATTAGGACCATATAATGTAAGTTTCTAOGGAAATCATTCGTGTG 1840
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1841 GTGAGTCAGGAACCTGTATTGTTTCCACCACGATAGCTGAAACATTCGCTATGCGCGT 1900
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
DB 1901 GAAATGTCCATGATGAGATTGAAAGCTGTCAGGAAGCCATGCTATGACTTT 1960
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
DB 1961 ATCATGAAATCGCTCATATAATTTGACACCCCTGTTGAGAGAGAGGGGCCCATGTCAT 2020
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 2021 GTGGGCAAGACAGAGGATCCCATTCACGTGCTGTTGTTGCGAACCCCAAGATCTTC 2080
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
DB 2081 CTGCTGGATGAGCCCGTCAGCTTGGACACAGAAAGCGAGCAGTGGTTTCAGGTGGCT 2140
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141

Db 2141 CTGGATAAGCCAGAAAAGGTCGGACCAACCATGTGATAGCTCATCGTTTGTCTACAGTT 2200
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyValaHis 161
Db 2201 CGTAATGCTGACGTCATCGCTGGTTTCGATGATGAGTCAATGTGTGGAGAGAGAAATCAT 2260
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrrSerLeuValMetSerGln----- 178
Db 2261 GATCAACTCATGAAGAAGAAAGGATTTACTTCAAACTTGTCAAAATGCCAGACAGCAGGA 2320
Qy 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrrSerThrGlu 195
Db 2321 AATGAAGTTGAATAGAAAATGCAGCTGATGAATCCAAAGTGAATGTATGCTTCGAA 2380
Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 2381 ATGCTCTTCAAAATGATCAAGATCCAGTCTAATAAGAAAAGATCAACTCGTAGAGTGTG 2440
Qy 210 Lys---SerAspPheIleAspLysAlaGluGlnSerThrGlnSerLysGluLysSerLeu 228
Db 2441 CGTGGATCACAAGCCACAGACAGAAAGCTTAGTACCAAGAGGCTCTGGATGAAGTATA 2500
Qy 229 ProGluValSerLeuLysIleLysLysLeuAsnLysProGluTrrProPheValVal 248
Db 2501 CCTCAGTTTCTTTTGGAGGATTATGAAGCTAAATTTAACTGAATGGCTTATTTGTT 2560
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2561 GTTGGTGTATTTTGTGCCATTATTAATGAGCGCTCGCAACCGATTTCACATATATTT 2620
Qy 269 AlalysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
Db 2621 TCMAAGATTATAGGGTTTTCACAGAAATTCATGATCTCTGAACACAAACGACAGATAGT 2680
Qy 288 GluIleTyrrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrrPheMet 307
Db 2681 AACTTGTHTTCACTAATTTGTCCTTACGCCCTTGGAAATTTCTTTTATATACATTTTCTT 2740
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Db 2741 CAGGGTTTCACATTTGGCAAGCTGGAGAGATCTCTACCAAGCGCTCCGATACATCGTT 2800
Qy 328 PheLysAlaMetLeuTyrrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
Db 2801 TTCCGATCCATGCTCAGACGAGATGTGAGTTGGTTGATGATCCCTTAAACACCACTGGA 2860
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
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Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2921 CTGTGCTGAATTAACCCAGATATAGCAAACTCTGGACAGCAATAATATATATCTTCTATC 2980
Qy 388 TyrrGlyTrrPheLeuMetThrPheLeuLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2981 TATGTTGGCAACTNACACTGTACTCTAGCAANTGTACCACTTACCATCTGCANTAGCAGGA 3040
Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnLeuLysHis 427
Db 3041 GTTGTGAATGAAAAATCTTCTCTGCAACAGCACTGAAAGATAAGAAAGAACTAGAAGGT 3100
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 3101 GCTGGGAAGATGCTTACTGAGACGATAGAAAACCTCCGACCGTGTGTTTCTTGTACTCAG 3160
Qy 448 GluLysAlaPheGluGlnMetTyrrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3161 GAGCAGAAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATCAGAAAACCTCTTGT 3220
Qy 468 LysLysAlaGlnIleIleGlySerCysTyrrAlaPheSerHisAlaPheIleTyrrPheAla 487
Db 3221 AGGAAGACACACATCTTTTGAATACATTTTCTTCCCTCACCCAGGCAATGATGATTTTCTC 3280

Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 3281 TATGCTGGATGTTTCCGGTTTGGAGCTACTTGGTGCCACATAAACTCATGAGCTTTGAG 3340
Qy 508 GlyMetPheIleValPheThrAlaIleAlaTyrrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3341 GATGTTCTGTAGTATTTTTCAGCTGTGTCTTTTGGTGCCATGCCCTGGGGAAGTCAGT 3400
Qy 528 ValLeuAlaProGluTyrrSerLysAlaLysSerGlyAlaAlaHisIleuPheAlaLeuLeu 547
Db 3401 TCATTGCTCTGACTATGCAAAAGCCAAAATATATCAGCAGCCACATCATCATGATCAAT 3460
Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3461 GAAAAAACCCCTTTGATTGACAGCTACAGCAGGAAGGCGCTTAATGCCGACACATTTGGA 3520
Qy 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrrProCysArgProAspValPheIle 587
Db 3521 GGAATGTCACTTTGTTGTTGAGTTGATTCAACTATCCCAACCGCCGACATCCCAAGTG 3580
Qy 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3581 CTTCAAGGACTGAGCCTGAGAGTGAAGAAGGCGCAGACCTGGCTCTGGTGGGAGCAGT 3640
Qy 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrrAspProValGlnGly 627
Db 3641 GGTGTGGGAGAGACACAGTGTCTCAGCTCTCTGGAGCGGTCTTACACCCCTTTGGCAGGG 3700
Qy 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGln 647
Db 3701 AAAGTCTGTGTTGATGCCAAAGAAATAAAGCGCACTGAATGTTTCAGTGGCTCCGAGCAC 3760
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Db 3761 CTGGGATGTTGTTCCAGAGGCGCCATCTCTGTTGACTGTCAGCATTCCTGAGAATTTGCC 3820
Qy 668 TyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAlaAla 687
Db 3821 TATGGAGACAAACAGCGCGGTGTGTCTACAGGAAGAGATCGTGGGCGCAGCAAGAGGCGC 3880
Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrrAsnThrGlnValGlyLeuLys 707
Db 3881 AACATACGCTTTCATTCGAGTCACTGCTCTAATAATATAGCACTAAAGTAGGAGACAA 3940
Qy 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3941 GGAACTCAGCTCTCTGTGCGCCAGAAACAAACGATTCGCCATAGCTCTGTCCTTGTAGA 4000
Qy 728 LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 4001 CAGCCTCATATTTTGTCTTGGATGAAGCCAGCTCAGCTCTGATACAGAAAGTGAAG 4060
Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 4061 GTTGTCCAGAGCCCTTGACAAAGCCAGAGAGCGCCACCTGCTATTGTGATTGTCTAC 4120
Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4121 CGCTCTCCACCATTCAGAAATGAGACTTAATAGTGTGTTTCAGAAATGCGAGAGTCAAG 4180
Qy 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrrPheLysLeuValAsn 807
Db 4181 GAGCATGGCAGCATCAGCAGCTGCTGGCAGAGAAAGGCACTATTTTTCATGCTCAGT 4240
Qy 808 AlaGlnSer 810
Db 4241 GTCCAGGCT 4249
RESULT 10
5206352-3
; Patent No. 5206352
; APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,

Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; FILING DATE: 01-AUG-1986
; PRIORITY DATE: 24-SEP-1986
; FILING DATE: 28-MAR-1986
; SEQ ID NO: 3
; LENGTH: 4669
5206352-3

Alignment Scores:
Pred. No.: 7.5e-278 Length: 4669
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 6 Gaps: 4

US-09-873-409-2 (1-812) x 5206352-3 (1-4669)
QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyArgAspHisIleGlyVal 21
DB 1781 GTTGATGGACAGATATTAGGACCAATTAATTAAGTTTCTACGGGAATCATTTGGTGTG 1840
QY 22 ValSerGlnGluProValLeuPheGlyThrIleSerAsnAsnIleValSerGlyArg 41
DB 1841 GTGAGTCAGGAACCTGATTGTTGGCCACCAGATAGCTGAAACCATTCGCTATGGCCGT 1900
QY 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaValAspPhe 61
DB 1901 GAAATGTCACATGATGAGATTGGAAGCTGTCAAGGAAGCCATTCCTATGACATT 1960
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
DB 1961 ATCATCAAACTGCCTCATAAATTTGACACCCCTGGTTGGAGAGAGAGGGGCCAGTTGAGT 2020
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 2021 GGTGGGCGAAGCAGAGAGATCGCATTCACGTCGCCCTGGTTCGCAACCCCAAGATCCCTC 2080
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
DB 2081 CTGCTGGATGAGCCACAGCTCAGCTTGGACACAGAAAGGAGCAGTGTTCAGGTGGCT 2140
QY 122 LeuGluLysAlaSerLysGlyArgThrIleValValAlaHisArgLeuSerThrIle 141
DB 2141 CTGGATAAGGCCAGAAAGGTCGACACCATTTGTGATAGCTCATCGTTTGTCTACAGTT 2200
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 2201 CGTAATGCTGACGTATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2260
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyThrSerLeuValMetSerGln----- 178
DB 2261 GATGAACCTCATGAAGAGAAAGCAATTTACTTCAAACTTTGTCAAAATGCAAGCAGCAGGA 2320
QY 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyThrGlu 195
DB 2321 AATGAAGTTGAATTAGAAATGCGCTGATGAATCCAAAGTCAAAAGTGAATGATCCCTTGGAA 2380
QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
DB 2381 ATGCTCTCAATGATTCAGATCCAGCTCAATTAAGAAAGAAAGATCACTCGTAGGAGTGTCTC 2440
QY 210 Lys---SerAspPheIleAspLysAlaGluSerThrGlnSerLysGluIleSerLeu 228
DB 2441 CGTGGATCAACAGCCCAAGACAGAAAGCTTAGTACCAAAAGAGGCTCTCGATGAAAGTATA 2500

QY 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248
DB 2501 CCTCCAGTTTCTTTTGGAGGATTATGAAGCTAAATTAATCTGAATGCGCTTATTTTGT 2560
QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
DB 2561 GTTGGTGTATTTTGGCCATTATAATGGAGCGCTGCAACAGCATTTTGCAATAATATT 2620
QY 259 AlalysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
DB 2621 TCAAGATTTATAGGGTTTTCACAGAAATTCATCTCTGAACCAAAACACAGCAATAGT 2680
QY 288 GlnIleTySerMetIlePheValIleLeuGlyValIleCysPheValSerTyPheMet 307
DB 2681 AACTGTGTTTCACTATTGTTTCTAGCCCTTGGAAATTTATTTTATTACATTTTCTCT 2740
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DB 2741 CAGGTTTTCATATTGGCAAGCTGGAGAGATCTCTCAACAGCGGCTCCGATACATGTT 2800
QY 328 PheLysAlaMetLeuTyGlnAspIleAlaThrPheAspGluLysGluAsnSerThrGly 347
DB 2801 TTCGATCCATGCTCAGACAGATGTGAGTTGGTTGATGACCTTAAACACCACTGGA 2860
QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
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DB 2981 TATGGTTGGCAACTTAACACTGTTACTCTTAGCAATTTGACCCATCATTTGCAATAGCAGGA 3040
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLysHis 427
DB 3041 GTTGTTCGAATGAATAATGTTCTCTGGACACACTGAAGATAAGAAAGAACTAGAGGT 3100
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
DB 3101 GCTGGAGATGCTGCTACTGAAGCAATAGAAACTTCCGACCGTGTGTTCTTTGACTCAG 3160
QY 448 GlyLysAlaPheGluGlnMetTyGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
DB 3161 GAGCAGAAATTTGAACATATATGATGCTCAGAGTTTGCAGGTACCATACAGAAACTCTTTG 3220
QY 468 LysLysAlaGlnIleIleGlySerCysTyThrAlaPheSerHisAlaPheIleTyPheAla 487
DB 3221 AGGAAAGCACACATCTTTGGAAATTAACATTTCTTCCACCGAGCAATGATGATTTTCC 3280
QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyLeuIleGlnAlaGlyArgMetThrProGlu 507
DB 3281 TATGCTGGATGTTTCCGGTTTGGAGCTTACTTGTGGCCACATAAATCATGAGCTTTGAG 3340
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyGlyAlaMetAlaIleGlyLysThrLeu 527
DB 3341 GATGTTCTGTAGTATTTTTCAGCTGTGTTCTTGTGGTCCATGGCCGGGCAAGTCACT 3400
QY 528 ValLeuAlaProGluTySerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
DB 3401 TCATTTGCTCTGCTATGTCACCAAGCAAAATATATCAGCAGCCCATCATCATGATCAT 3460
QY 548 GlnLysLysProAsnIleAspSerArgSerGlnGluLysLysLysProAspThrCysGlu 567
DB 3461 GAAAAACCCCTTTGATTGACAGCTACAGCAGGAAGGCTTAATGTCGCCAACACATTTGAA 3520
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyProCysArgProAspValPheIle 587
DB 3521 GGAATGTACATTTGTTGGAAGTTGTTTCAACTATCCACCCGACCGGACATCCAGTGG 3580

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; LENGTH: 8630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proviral
; OTHER INFORMATION: plasmid DNA
; NAME/KEY: misc feature
; LOCATION: (1)..(160)
; OTHER INFORMATION: plasmid backbone (pUC)
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; NAME/KEY: 3'-LTR
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; OTHER INFORMATION: retroviral expression vector SFbeta71m4
US-09-306-417-1

Alignment Scores:
Pred. No.: 2,23e-277 Length: 8630
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
Gaps: 4

US-09-873-409-2 (1-812) x US-09-306-417-1 (1-8630)
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Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 2636 GTGAGTCAGGAACCTGTATTGTTGCCACCACGATAGCTGAAACACATTCGCTATGGCCGT 2695
Qy 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 2696 GAAATGTCACCATGATGAGATTGAGAAAGCTGTCAAGGAAGCCANTGCCATGACTTT 2755
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 2756 ATCATGAAACCTGCCTCATAAATTTGACACCCCTGTTGGAGAGAGAGGGCCGCGATTGAGT 2815
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 2816 GGTGGGAGAGAGAGAGAGATGCCATTGCACTGCCCTGGTTTCGCAACCCCAAGATCCTC 2875
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Qy 122 LeuGlnLysAlaSerLysGlyArgThrThrIleValValAlaAlaHisArgLeuSerThrIle 141
Db 2936 CTGGATAGGCCAGAAAGGTCGAGCCACCAATGTGTAGTCTCATCGTTTGTCTACAGTT 2995

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Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGlnLysGlyAlaHis 161
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Db 3056 GATGAACCTCATGAACAGAAAGCGATTTACTTCANACTTGTCAANTGCAGACAGCAGGA 3115
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Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
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Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507

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QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaA 121
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RESULT 14

US-08-793-610-6

Sequence 6, Application US/08793610

Patent No. 5858744

GENERAL INFORMATION:

APPLICANT: BAUM, Christopher

APPLICANT: STOCKING-HARRIS, Carol

APPLICANT: OSTERAG, Wolfram

TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF

TITLE OF INVENTION: FOR GENE TRANSFER

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

STREET: 655 Fifteenth Street N.W. Suite 330

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,610

FILING DATE: 07-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 31 973.8

FILING DATE: 08-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 03 952.1

FILING DATE: 07-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03175

FILING DATE: 10-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Beiman, Richard J.

REGISTRATION NUMBER: 39,105

REFERENCE/DOCKET NUMBER: P1614-7007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-5000

TELEFAX: (202)638-4810

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 9318 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA

US-08-793-610-6

Alignment Scores:

Pred. No.: 2,556-277 Length: 9318

Score: 2436.00 Matches: 466

Percent Similarity: 76.79% Conservative: 165

Best Local Similarity: 56.62% Mismatches: 177

Query Match: 59.72% Indels: 14

Gaps: 4

US-09-873-409-2 (1-812) x US-08-793-610-6 (1-9318)

Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21

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Db 3672 AATGAAGTTGAATAGAAAATGCAGCTGATGAATCCAAAAGTGAATGATGCTTGGAA 3731

Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209

Db 3732 ATGCTTCAATATGATTCAGATCCAGTCTTAATAAGAAAAGATCACTCGTAGGAGTGT 3791

Qy 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluLeuSerLeu 228

Db 3792 CGTGGATCACAAAGCCCAAGACAGACAGAGCTTAGTACCAAGAGGCTCTGATGAAAGTATA 3851

Qy 229 ProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248

Db 3852 CTCCAGTTTCTCTTTGGAGGATATGAGCTAAATTTAACTGAATGGCCCTTATTTGTT 3911

Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268

Db 3912 GTTGTGTATTTTGTGCCATATAATGGAGGCTGCAACAGCATTTGCAATAATATT 3971

Qy 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287

Db 3972 TCAAGATATATAGGGGTTTTTACAAGAAATTGATGATCTGAAACAAACACGACAGATAGT 4031

Qy 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307

Db 4032 AACTGTTTTCATTTGTTTCTAGCCCTTGGAAATATTCTTTTATACATTTTCTCTT 4091

Qy 308 GlnGlyLeuPheTyrGlyArgAlaGlyLeuLeuThrMetArgLeuArgHisLeuAla 327

Db 4092 CAGGGTTTCACATTTGGCAAGCTGGAGATCTCTCACCAAGCGCTCCGATACATGTT 4151

Qy 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347

Db 4152 TTCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGATGCCCTTAAACACCACTGGA 4211

Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367

Db 4212 GCATTTGACTACAGGCTCGCCAATGATGCTGCTCAAGTTAAAGGGGCTATAGTTCCAGG 4271

Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387

Db 4272 CTTCGTGTAATTTACCAGAAATAGCAATCTTGGGACAGGAATTAATATATATCTTCATC 4331

Qy 388 TyrGlyTyrPheGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407

Db 4332 TATGCTGGCACTAAACACACTGTTACTCTTACCAATTTGATCCCATCTTGCATATAGCAGGA 4391

Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427

Db 4392 GTTGTGTAATGAAATGTTGTTCTGGCAACGACTGAAAGATAGAAAGAACTAGGAAGGT 4451

Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447

Db 4452 GCTGGGAAGATCGTACTGAGCAATAGAAACCTTCGGAACCGTGTCTTCTTGTGACTCAG 4511

Qy 448 GlnLysAlaPheGluGlnMetThrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467

Db 4512 GAGCAGAAGTTTGAACATATGTTATGCTCAGAGTTTGCAGTTTGCAGTACACAGAAACTCTTTG 4571

Qy 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487

Db 4572 AGGAAGCACATCTTTGAAATTCATTTCTTCCACGAGCAATGATGTTATTTTC 4631

Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507

Db 4632 TATGCTGATGTTTCCGGTTTGGAGCTTACTTGTGGGCACATAAACTCATGAGCTTGGAG 4691

Qy 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527

Db 4692 GATGTTCTGTTGATTTTTCAGCTTGTGTTTGTGTCCTATGCGCGTGGGGCAGTCAGT 4751

Qy 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547

Db 4752 TCATTTGCTGCTGATGTCGCAAGCAAAATATPCAGCAGCCACATCATCATCATCAT 4811

Qy 548 GlnLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567

Db 4812 GAAAGAAACCCCTTTGATGTCAGCTATCAGCAGGAGGCTTAATGCGGAACACATTCGAA 4871

Qy 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587

Db 4872 GGAATGFCACATTTGGTGAAGTTGTTTCACTATCCACCCGACCGGACATCCAGTG 4931

Qy 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607

Db 4932 CTTGAGGACATGACCTGGAGGTGAAGAGGGCCAGCGTGGCTCTGGTGGCAGCAGT 4991

Qy 608 GlyCysGlyLysSerThrSerValGlnLeuGlnArgLeuTyrAspProValGlnGly 627

Db 4992 GGCTGTGGAGAGACACACAGCTGCTCAGCTCTGGAGGGTCTACGACCCCTTGGCAGGG 5051

Qy 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnThrLeuArgSerGln 647

Db 5052 AAAGTGTCTGTGATGCAAGAAATAAAGCGACTGAATGTTTCACTGGCTCCGAGCACAC 5111

Qy 648 IleAlaIleValProGlnGluProValIleuPheAsnCysSerIleAlaGluAsnIleAla 667

Db 5112 CTGGGATCGTGTCCAGGAGCCCTCTGTTTACTGACGATTTGCTGAGACATGCCC 5171

Qy 668 TyrGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsnAlaAla 687

Db 5172 TATGAGACAAACACCGGGTGTGTACAGAGAGATCGTAGGGCAGCAAGAGAGGCC 5231

Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLys 707

Db 5232 AACATATGCTCTTCATCGAGTCTCTGCTTAATAATATAGCATAAAGTAGGAGACAAA 5291

Qy 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727

Db 5292 GGAATCAGCTCTCTGGTGGCCAGAACACGCAATTCGCATAGCTCTGGCCCTTGTAGA 5351

Qy 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnSerGluLys 747

Db 5352 CAGCCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGATACAGAAAGTGAAG 5411

Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767

Db 5412 GTTGTCCAGAGACCTTGAACAAAGCCAGAGAGGCGCCACTCTGATTTGATTTGCTCAC 5471

Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787

Db 5472 CCCTGTCCACCATCCAGATCCAGACTTAATAGTGGTGTTCAGAAATGGCAGACTCAAG 5531

Qy 788 GluGlnGlyThrHisGlnIleLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807

Db 5532 GAGCATGGCAGCATCAGCAGCTGTGGCAGAAAGGCATCTATTTTCAATGCTCAGT 5591

Qy 808 AlaGlnSer 810

Db 5592 GTCCAGGCT 5600

RESULT 15

US-09-120-513-1
 ; Sequence 1, Application US/09120513
 ; Patent No. 6025160
 ; GENERAL INFORMATION:
 ; APPLICANT: Brun, Kimberly
 ; APPLICANT: Chenery, Richard
 ; APPLICANT: Ellens, Harma
 ; APPLICANT: Field, John
 ; APPLICANT: Yue, Lin
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
 ; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDR1B2 AND
 ; TITLE OF INVENTION: SCREENING METHODS THEREOF
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY:
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/120,513
 ; FILING DATE: 22-JUL-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: King, William T.
 ; REGISTRATION NUMBER: 30,954
 ; REFERENCE/DOCKET NUMBER: GP50008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5015
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4233 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; US-09-120-513-1

Alignment Scores:
 Pred. No.: 2,956-275 Length: 4233
 Score: 2413.50 Matches: 467
 Percent Similarity: 76.03% Conservative: 158
 Best Local Similarity: 56.81% Mismatches: 180
 Query Match: 59.17% Indels: 17
 DB: 3 Gaps: 5

US-09-873-409-2 (1-812) x US-09-120-513-1 (1-4233)

Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21

Db 1376 ATCGACGGACAGCAGCATCAGGACCATCAATGTGAGGTATCTCGGGAATCATTTGGGGTG 1435

QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnIleIysTyrGlyArg 41
DB 1436 GTGAGTCAGGAACCCGCTGCTGTTCACACAGATTCGCCAAACATTCGCTATGCGCGA 1495
QY 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
DB 1496 GAAACGTCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1555
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
DB 1556 ATCATGAAATGCCCCACCAATTAACACCTCGGTGGTGAGAGGGCGCGAGCTGAGT 1615
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 1616 GGGGAGCAGAAACAGAGGATCGCCATTGCCCGGCGCTGCTCGGACCCCAAGATTCCT 1675
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
DB 1676 TTGTTGGATGAGCGCACGTCAGCTTGGACACAGAAAGCGCGCTGCTGCTGCTGCTGCT 1735
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
DB 1736 CTGGATAAGGCTAGAGAGCGCGACCATCTGATGATGATGATGATGATGATGATGATG 1795
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1796 CGCAATGCTGAGCTCATTCGTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1855
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIleLys 181
DB 1856 GAAGAGCTCATGAAGAGAGGCGCATTTACTTCAAACTGTGATGATGATGATGATGATGAT 1912
QY 182 LysAlaAspGluGlnMetGluSerMetThrThrThrThrThrThrThrThrThrThr 201
DB 1913 GGAATGAATGAACACAGCAAGAAATATGCTTATGATCCCAAGTGACACTGGTGCCTCT 1972
QY 202 ProLeuHisSerValLysSerLysSerLysSerPheIleAspLysAla----- 217
DB 1973 GAGTTGACTTCAGAAAAATCA---AAATCTCCTTTAATAAGGAGATCAATTCGACAGAGT 2029
QY 218 -----GluGluSerThrGlnSerLysGlu-----IleSer 227
DB 2030 ATCCACAGAAAGACAGACAGAGAGAGACTTAGTTCCAAAGAGAGATGGATGAGAGAT 2089
QY 228 LeuProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrProPheVal 247
DB 2090 GTGCCCTATGCTTCCTTTTGGCAGATCCCAAAGCTAAATATTAGTGAATGGCCCTATTTA 2149
QY 248 ValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleLe 267
DB 2150 GTGTGGGTGTACTTGTGCTGTATAAATGGGTGATACAAACCGAGTGTTCGCTATAGT 2209
QY 268 PheAlaLysIleIleThrMetPheGly---AsnAsnAspLysThrThrLeuLysHisAsp 286
DB 2210 TTTCAAAGATTTGAGGGGTTTTTTCAGAGACGACGACCATGAACCAACCAACGGAAT 2269
QY 287 AlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPhe 306
DB 2270 TGTAACTTGTTCCTCTCTCTCTGTCATGGGAATGATTTCTTTTGTACGTACTTC 2329
QY 307 MetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeu 326
DB 2330 TTTCAGGCTTCACATTTGGCAAGCTGGAGATCTCTCACCACGAGCTCGATACATG 2389
QY 327 AlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThr 346
DB 2390 GTCTTCAAAATCCATGCTGCAGCAGGATATAAGCTGGTTTGTATGACCATATAAACCACT 2449
QY 347 GlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyValaThrGlySer 366
DB 2450 GGCTGCTGCTACACGAGCTGCTAGTACGCTTCTAATGTTTAAAGGGGCTATGGGCTCC 2509

QY 367 ArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPhe 386
DB 2510 AGGCTTGCTGTAGTTTACCCAGAAATGTAGCAAACTTGGCAGAGAAATATCTTATCTTTA 2569
QY 387 IleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThr 406
DB 2570 GTCATGGCTGCAGCTTACACTTTTACTTGTAGTAATTATACCACTCATTTGCTTGGT 2629
QY 407 GlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLys 426
DB 2630 GGAATTATTGAAATGAAACTGTTGCTGCTCAAGCCTTGAAGGACAGAAAGAGCTAGAG 2689
QY 427 HisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThr 446
DB 2690 ATCTCTGGGAAGATGCTACAGAGCAATGGAACCTCCGCACTGTTGCTCTCTTGACT 2749
QY 447 ArgGlnLysAlaPheGluGlnMetTyrGluLeuMetLeuGlnThrGlnHisArgAsnThr 466
DB 2750 AGGAGCAGAAATTTGAACATATATGATGCCAGAGCTTGCAGATACCATCAGAAATGCT 2809
QY 467 SerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPhe 486
DB 2810 TTGAGAAAGCACAGCTTTTGGGATCACCTTCGCTTCCAGGCGCATGATTATTTT 2869
QY 487 AlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrPro 506
DB 2870 TCCTATGCTGCTGCTTTCGCTGCTTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2929
QY 507 GluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThr 526
DB 2930 GAAATGTATGTTGGTATTTCCTGCTGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 2989
QY 527 LeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeu 546
DB 2990 AGTTCAATTCGCTCTGACTACGCGAAGCCAAAGTCTCAGCATCCACATCATCAGGATC 3049
QY 547 LeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCys 566
DB 3050 ATTGAGAAATCCCGAGATTCAGAGCTTACAGCAGCGAGGCTTGAAGCCTTAATTTGGTTA 3109
QY 567 GluGlyAsnLeuGluPheArgGluValSerPheTyrProCysArgProAspValPhe 586
DB 3110 GAAGGAATGTGAATTTAATGAGTCTATGTTCAACTATCCACCCGACCCACATCCCA 3169
QY 587 IleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySer 606
DB 3170 GTGCTTCAGGAGCTGAGCTTCGAGTGAAGAGGGGCAACGCTTCGCTGCTGGGCGAGC 3229
QY 607 SerGlyCysGlyLysSerThrSerValGlnLeuGlnArgLeuTyrAspProValGln 626
DB 3230 AGTGGCTCGGGAAGAGTACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3289
QY 627 GlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnThrLeuArgSer 646
DB 3290 GGAACAGTGTTCATAGATGGCAAGAAATAAACCACTCAACGCTCCAGTGGCTCCGCGCC 3349
QY 647 GlnIleAlaIleValProGlnProValLeuPheAsnCysSerIleAlaGluAsnIle 666
DB 3350 CACTTGGGCAATTTGTCCTCCAGAGGCCATCTCTGTTGACTGTCAGCATCACCAGAACATC 3409
QY 667 AlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAla 686
DB 3410 GCCTACGGAGACACAGCCGCTGCTGCTCATCAGGAGATCGTGAGGCGCCAGGCGAG 3469
QY 687 AlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeu 706
DB 3470 GCCAACATCCACCACTCATCGACTCTGCTGAGAAATACCAACACAGAGTGGGAGAC 3529
QY 707 LysGlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeu 726
DB 3530 AAAGGAGCTCAGCTGTGGCGGCGAGAGCGCATCGCCATCGCGCGCGCTCGTC 3589
QY 727 GlnLysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnSerGlu 746

Db	3590	AGACAGCCTCACATCTTACTTCTGGATGAAGCGACATCAGCTCTGGATACGGAGAGTGAA	3649
Qy	747	LysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThr	766
Db	3650	AAGTCTCTCCAGGAAGCGCTGGACAAAGCCAGGAGCGCCACCTGCATTGTGATCGCG	3709
Qy	767	HisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIle	786
Db	3710	CACCGCTGTCCACCATCCAGAACGCAGACTTGTATCTGTGATTTCAGAACGCCAGGTC	3769
Qy	787	LysGlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuVal	806
Db	3770	AAGGAGCACCGCACCCACCCAGCAGCTGTGCGCCAGAAAGGCATCTATTTCGATGGTT	3829
Qy	807	AsnAla	808
Db	3830	CAGGCT	3835

Search completed: June 25, 2004, 01:42:10
Job time : 285 secs

QY 2644 AATGACAGTGAAGGTGGTTTCAGCATGCCCTTGATAAAGCCAGGACGGAGGACATGC 2703
 Db 3688 ACAGAAAGTGAAGGTGGTTTCAGCATGCCCTTGATAAAGCCAGGACGGAGGACATGC 3747
 QY 2704 CTAGTGGTCACTCAGAGGCTCTCTGCAATTGAGAACGACAGATTGATAGTGGTCTGAC 2763
 Db 3748 ATTGTGATTGCTCAGGCTGTCCACCATCCAGATGACACTTAATAGTGGTGGTTTCAG 3807
 QY 2764 AATGGAAGATAAGGACAGGACGACATCATCAAGGCTCTGAGAAATCGAGCATATAT 2823
 Db 3808 AATGGCAGAGTCAAGGAGCATGACGACATCAGCAGCTGTGACAGAAAGGACATCTAT 3867
 QY 2824 TTTAAGTTAGTGAATGCACAGTCAAG 2848
 Db 3868 TTTTCAATGCTCAGTGTCCAGGCTG 3892

RESULT 2

US-08-181-471-2
 ; Sequence 2, Application US/08181471
 ; Patent No. 5641508
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Lingna
 ; APPLICANT: Lisko, Valeryi K.
 ; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
 ; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Thomas Fitting
 ; STREET: 12526 High Bluff Drive, Suite 300
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92130
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/181.471
 ; FILING DATE: 13-JAN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/041,553
 ; FILING DATE: 02-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: ANT0029P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-792-3680
 ; TELEFAX: 619-792-8477
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 425..4267
 ; US-08-181-471-2

Query Match 36.1%; Score 1030.2; DB 1; Length 4646;
 Best Local Similarity 62.2%; Pred. No. 2.5e-288;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
 QY 166 ATTATTGATAAGAAACCAGTATAGATAACTTTTCCACAGCTGGATATAAACCTGAATCC 225

Db 1526 ATAAATTGATAAAGCCAGTATTTCAGAGCTATTCCGAGAGTGGGCACAAACAGATAAT 1585
 QY 226 ATAGAAGGAAGTGTGGAATTTTAAATTTTCTTTCAATTTATCCATCAAGACCATCTATC 285
 Db 1586 ATTAAAGGGAATTTGGAATTTTCAATTTTCTTTCAATTTATCCATCAAGACCATCTATC 1645
 QY 286 AAGATTCTGAAAGGTCTGAATCTCAGAATTAAGTCTGGAGACACAGTCCCTTTGGTGGCT 345
 Db 1646 AAGATCTTGAAGGCTGAACTGAGGTGACAGAGGAGGACAGCGTGGCCCTGGTTGGA 1705
 QY 346 CTCATATGGCAGTGGGAAGATACGGTAGTCTCAGCTTCTGCAAGGTTATATATATCGGAT 405
 Db 1706 AACAGTGGCTGTGGGAAGAGACAAACAGTCCAGCTGATGACAGGCTCTATGACCCACA 1765
 QY 406 GATGGCTTTATCATGTGTGATGAGATGACATCAGAGCTTTAAATGTGCGGCAATATCA 465
 Db 1766 GAGGGATGGTCACTGTTGATGACAGGATATTAGACCATTAATGTAAGGTTTCTACGG 1825
 QY 466 GACCATATTGGAGTGGTTAGTCAAGAGCTGTTTGTGGGACCAACCAACAGTAAACAT 525
 Db 1826 GAAATCAATGGTGTGGTGAAGTCAAGAACTGTAATTTTGGCCACCAAGATAGCTGAAAC 1885
 QY 526 ATCAAGTATGGACGAGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 585
 Db 1886 ATTGCTATGGCCGTAAGAAATGTCCATGATGATGATGATGATGATGATGATGATGATG 1945
 QY 586 AATGGTATGATTTTATCATGAGGTTTCTTAATAATTTTAAATTTTAAATTTTAAATTT 645
 Db 1946 AATGGCTATGACTTTTATCATGAACTGCTCATAAATTTTACACCTGTTGGAGAGA 2005
 QY 646 GGAGCTCAATGATGAGTGGAGGAGGAGAAACAGAGATGCGAATTTGCTGCTGCTTATGCA 705
 Db 2006 GGGGGCCAGTTGAGTGGTGGGAGAGAGAGAGATGCGCAATTTGACAGCTGCTGCTGCTG 2065
 QY 706 AACCCCAAGATTTCTGATTTTATGATGAGGCTAGTGTGCTGCTGCTGCTGCTGCTGCTG 765
 Db 2066 AACCCCAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2125
 QY 766 GCTGTTCAAGTGCATCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825
 Db 2126 GTGGTTTCAAGTGGCTCTGATTAAGGCGCAGAAAGGTGCGACCACTTTGATGATGAT 2185
 QY 826 CGACTTTCTACTATTTCGAAAGTGCAGATTTGATTTGATGACCTTAAAGGATGGAATGCTG 885
 Db 2186 CGTTTGTCTACAGTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2245
 QY 886 GAGAAAGGAGCAGTCTGCAACTTAATGGCAACAGAGGCTCTATATTTATTTATTTATTT 945
 Db 2246 GAGAAAGGAAATCATCATGAACTCATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2305
 QY 946 TCACAGGATATTAAAGAGCTGATGACAGATGAGGATGATGATGATGATGATGATGATG 997
 Db 2306 ATGCAGACAGCAGGAAATGAAGTTGAATTTAGAAAATGTCAGCTGATGATGATGATG 2365
 QY 998 -----CTGAAAGAAAGACCAACTCACTTCTCTGCACTCTGTGAAAGAGCATCA--- 1045
 Db 2366 ATTGATGCTTGGAAATGCTTCAATGATTTCAAGATCCAGTCTAATAAGAAAAGATCA 2425
 QY 1046 -----AGTCAGACTTCAATGACAGGCTGAGGAATCCACCCATCT 1086
 Db 2426 ACTCGTAGGAGTGTCCGTGGATCAAGGCCCAAGACAGAAAGCTTAGTACCAGAGGCT 2485
 QY 1087 AAAGACATAAGTCTTCTGTAAGTCTCTATTTAAATTTTAAAGTTAAAGTTAAAGTTAA 1146
 Db 2486 CTGGATGAAGTATGATCTCCAGTTTCTTTTGGAGGATTTATGAGCTAATTTAATCTGA 2545
 QY 1147 TGGCCTTTTGTGTTCTGGGAGCATTTGCTTCTGTTCTAAATGGAATCTGTTCTATTCAGTA 1206
 Db 2546 TGGCCTTTTGTGTTCTGGGAGCATTTGCTTCTGTTCTAAATGGAATCTGTTCTATTCAGTA 2605
 QY 1207 TTTTCCATCATCTTTCGAAATTAATTAACCATGTTTGGAAATTAATGATATAAACCATTA 1266

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1167:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: G187468
 US-09-023-655-1167

Query Match 36.1%; Score 1030.2; DB 4; Length 4646;
 Best Local Similarity 62.2%; Pred. No. 2.5e-288;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

QY 166 AATTATGATGAAGAAACCCAGATATAGATAAATCTTTCCACAGCTGGATATAAACCCTGAATCC 225
 DB 1526 ATAATTGATATAAGCCCAAGTAATGACAGCTATTCGAGAGTGGGCGACAAACAGATAAT 1585

QY 226 ATGAAGGAACCTGGGAATTTAAATGTTTCTTCAATATATCCATCAAGACCAATCTATC 285
 DB 1586 ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTTACCCTATCTCGAAAGAAAGTT 1645

QY 286 AAGATTCGAAAGCTGTAATCTCAGAAATTAAGTCTCGGAGAGACAGTCGCTTGGTGGT 345
 DB 1646 AAGATCTTGAAGGCTTGACCTGAAGTGCAGAGTGGGCGACAGCTGGGCTTGGTGA 1705

QY 346 CTCGAATGGCAGTGGGAAGATGACGTAGTCCAGCTTCGAGAGGTTATATGATCCGGAT 405
 DB 1706 AACAGTGGCTGTGCGAAGAGACAAACAGTCGAGCTGATGAGAGGCTCTATGACCCACCA 1765

QY 406 GATGGCTTATCATGTTGGATGAGATGACATCAGAGCTTTAAATGCGGCAATTATGA 465
 DB 1766 GAGGGATGTTGAGTTGATGAGCAGGATATGAGACCAATAATGTAAGGTTTCTACGG 1825

QY 466 GACCATATGCGAGTGGTGTAGTCAAGACCTGTTTGTTCGGGACCCACCAATCAGTAACAT 525
 DB 1826 GAAATCATGTTGGTGGTGGTCAAGAACCTGTATGTTGCCACCAAGATAGTGAAGAAC 1885

QY 526 ATCAAGTATGACAGATGATGACTGATGAGAGATGAGAGAGCAGCAGCAGGAGCA 585
 DB 1886 ATTGCGTATGCGCTGGAATGTGACCATGATGAGATGAGAAAGCTGTCAAGGAAAGCC 1945

QY 586 AATCGGTATGATTTATCATGGAGTTTCCTAAATAATTTAATACATTTGGTGGGGAATAA 645
 DB 1946 AATGCGTATGACTTTATCATGAACTCCCTCATATAATTTGACACCTGTTGAGAGAGA 2005

QY 646 GGAGCTCAAAATGATGAGGAGGCGAAACAGAGGATGCAATGCTGCTGCTTGTGTTGA 705
 DB 2006 GGGGCCCAAGTTGATGTTGGGCGAGAGCAGAGGATGCCAATTCGACGTGCTGCTGCTGC 2065

QY 706 AACCCCAAGATTCGTATTTAGATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
 DB 2066 AACCCCAAGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2125

QY 766 GCTGTTCAAGCTGCACTGGAAGAGGCGAGCAAGAGTGGGACTCAATCGTGGTAGCACAC 825
 DB 2126 GTGGTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2185

QY 826 CGACTTCTACTATTCGAAGTGCAGATTTGATGTCGACCTTAAGAGTGAAGTGGAGTGGCG 885
 DB 2186 CGTTTGTCTACGTTCTGATTAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245

QY 886 GAGAAAGGAGCAGATGCTGAATTAATGCGAAACAGAGTCTATATTTATTCACCTTGTGATG 945
 DB 2246 GAGAAAGGAAATCATGATGAATCATGAAAGAGAGAGGCAATTTACTTCAAACTGTGACA 2305

QY 946 TCACAGGATATTAAGAGCTGATGAACAGATGAGTCAATGATATTTCTTA 997
 DB 2306 ATGCAAGCAGCAGGAATGAAGTTGAATTGAGAAATGACGCTGATGAATCCAAAGTGAA 2365

QY 998 -----CTGAAAGAAAGACCAACTCACTTCTCTGCACTCTGTGAGAGAGCATCA--- 1045
 DB 2366 AATTGATGCTTGGAAATGTCTTCAATGATTCAGATCCAGTCTAATAAGAAAAAGATCA 2425

QY 1046 -----AGTCAGACTTCAATTTGCAAGGCTGAGCAATCCACCCAACTCT 1086
 DB 2426 ACTGTAGAGAGTGTGCGTGATCAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT 2485

QY 1087 AAAGAGATAAGTCTTCTGAAAGTCTCTATTAATAAAATTTTAAAGTAAACAGCTGAA 1146
 DB 2486 CTGGATGAAAGATATACCTCCAGTTTCTTTGGAGGATATGAAGCTAAATTTAACTGAA 2545

QY 1147 TGGCTTTTGTGTTCTGGGAGCATGGCTTCTGTTCTAAATGGAAGTCTTCTATCCAGTA 1206
 DB 2546 TGGCTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2605

QY 1207 TTTTCCATCATCTTTGCAAAAATTAATAACATGTTTGGAAATTAATGATAAAACCAATTA 1266
 DB 2606 TTTGCAATAATATTTCAAGATTAAGGGTTTTCACAGAAATGATGATCTCTGAAACA 2665

QY 1267 AAG---CATGTGACAGAAATTTATTCATGATATTCGTCTATTTTGGGTGTTATTTGCTTT 1323
 DB 2666 AAACGACAGAAATGATTAATTTGTTTCTATTTTCTAGCCCTTGGAAATTAATTTCTTTT 2725

QY 1324 GTCAGTTATTTCAATGACGGGATTTATTTACGCGACAGCAGGGGAAATTTTAAACGATGAA 1383
 DB 2726 ATTACATTTTCTTTCAGGGTTTCAATTTGCAAGCTGGAGAGATCTCTACCAAGCGG 2785

QY 1384 TTAAGACATCTGGCTTCAAGCCATGTTATATCAGGATATTTGCTGTTGTTGATGAAAAG 1443
 DB 2786 CTCGATACATGTTTTCGATCCATGCTCAGACAGGATGTTGATGTTGTTGATGACCTT 2845

QY 1444 GAAACAGCACAGGAGGCTTGACAAATATTTAGCCATAGATATAGCAAAATTTCAAGGA 1503
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QY 1504 GCAACAGTTTCAGGATGGCTCTTAAACAAAAATGCAACTTAAACATGGAGCTTTTCAGTT 1563
 DB 2906 GCTATAGTTTCAGGCTTCTGTAATTAACCCAGAAATATAGCAAACTTGGGACAGGAATA 2965

QY 1564 ATCAATTCCTTTATATGATGAGGAGATGACATCTCTGATTTCTGAGTATTTCTCCAGTA 1623
 DB 2966 ATTATATCTCTCACTATGTTGGCACTAAACACTGTTACTCTTAGCAATTTGATCCATC 3025

QY 1624 CTTGCGTGACAGGAATGATTTGAAACCGCAGCAATGACTGGATTTGCCAACAAAGATAAG 1683
 DB 3026 ATTGCAATAGCAGGAGTTGTTTGAATGAAATGTTGCTGGACAAGCACTGAAAGATAAG 3085

QY 1684 CAAAGAACTTAAGCATGCTGGAAGAGATAGCACTGAGCTTTGAGAGATATAGTACTATA 1743
 DB 3086 AAAGAACTAAGAGGCTGCGGAAGATCGCTACTGAAGCAATAGAAAACTTCCGAAACGTT 3145

QY 1744 GTGTCAATTAACAGGAAAGAAAGCCCTTCGAGCAAAATGATGAAGAGATGCTTCAGACTCAA 1803
 DB 3146 GTTTCTTGTGACTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCA 3205

QY 1804 CACAGAAATACCTCGAAGAAAGCAAGATTAATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
 DB 3206 TACAGAAACTCTTTGAGGAAAGCACATCTTTGGAATTAACATTTTCTTCCATCCAGGCA 3265

QY 1864 TTTATATAATTTGCTATGACGCGGTTTCCATTTGGAGCTTATTTAATTTCAAGCTGA 1923
 DB 3266 ATGATGATTTTCTTATGCTGAGTGTTCGCTTTGGAGCTTACTTGTGGGCACATATA 3325

QY 1924 CGAATGACCCAGAGGCGATGTTCAATGTTTATGCAATTTGCAATGATGAGACTATGGCC 1983
 DB 3326 CTCATGAGCTTTGAGGATGTTCTGTAGTATTTTTCAGCTGTTGTTGCTTTTGGTCCATGCC 3385

QY 1984 ATCGGAAAGACGCTGTTTGGCTCTGTAATTTCCAAAGCCAAATCGGGGCTCGCAT 2043
 DB 3386 GTGGGCAAGTCAGTTCTATTTGCTCTCTGACTATGCAAGCCAAATATCAGACGCCAC 3445

2044	QY	CTGTTTGCCTTGTGTGAAGAAGAAACCAATATATAGACAGCGCAGTCAAGNAGGGAAG	2103	QY	TTTCTTATCCATCTGCG
3446	DB	ATCATCATGATCAATGAAAAACCCCTTTGATTGACAGCTACGACGGAAGCCCTAAATG	3505	DB	TTTCTTATCCATCTGCG
2104	QY	CCAGACACATGTGAAGGGAAATTTAGAGTTTCGAGAAGTCTCTTTCTTCTATCCATCTGCG	2163	QY	TTTCTTATCCATCTGCG
3506	DB	CCGAAACACATTCGAAAGGAATGTCAATTTGTTGAGTTGTTATTTCAACTATCCACCCGA	3565	DB	TTTCTTATCCATCTGCG
2164	QY	CAGATGTTTTTCACTCTCGTGGCTTATACCTCAGTATTGAGCGAGAAAGACAGTAGCA	2223	QY	TTTCTTATCCATCTGCG
3566	DB	CCGGACATCCCACTGCTTCAGGCACTCAGCCTCGAGGTGAAGAAGGCCACAGCGCTGGCT	3625	DB	TTTCTTATCCATCTGCG
2224	QY	TTTGTGGGAGCAGCGCTGTGGGAAGACATTCCTGTTCAACTCTCTGACAGACATTTAT	2283	QY	TTTCTTATCCATCTGCG
3626	DB	CTGTGTGGGAGCAGTGGCTGTGGGAAGACAGTGGTCCAGTCTCTGGAGCGGTCTTAC	3685	DB	TTTCTTATCCATCTGCG
2284	QY	GACCCCGTCAAGGACAAGTGTCTTTTGATGTGTGATGCAAAAGAAATGAAATGTACAG	2343	QY	TTTCTTATCCATCTGCG
3686	DB	GACCCCTTGGCAGGGAAGTGTCTGTGATGTGCAAGAAATAAAGCGACTGAATGTTTCA	3745	DB	TTTCTTATCCATCTGCG
2344	QY	TGGCTCCGTTCCCAATAGCAATCGTTCTCTAAGAGCCTGTGCTCTTTCAACTCCAGCAT	2403	QY	TTTCTTATCCATCTGCG
3746	DB	TGGCTCCGAGCACACTCGTGGCACTCGTGTCTCCAGGAGCCATCTCTTTTCACTGCA	3805	DB	TTTCTTATCCATCTGCG
2404	QY	GCTTGACAAACATCCCTATGTGTGACAAACAGCCGTGTGTGCAATTAGATGAGATCAAGAA	2463	QY	TTTCTTATCCATCTGCG
3806	DB	GCTTGAGAACATTCCTTATTGAGAACACAGCCGGTGTGTTCACAGNAGATCTGTAGS	3865	DB	TTTCTTATCCATCTGCG
2464	QY	GCCGCAATTCAGCAAAATTCATCTCTTTTATGAAAGTCTCCCTCAGAAATACAAACA	2523	QY	TTTCTTATCCATCTGCG
3866	DB	GCAGCAAGAGGAGCCAAACATACATGCTTCATCGAGTCACTGCTTAATAATATAGCACT	3925	DB	TTTCTTATCCATCTGCG
2524	QY	CAAGTTGGACTGAAGAGGACAGCTTTCTGGCGGCCAGAAACAAAGACTAGCTATTGCA	2583	QY	TTTCTTATCCATCTGCG
3926	DB	AAAGTAGGAGACAAAGGAACCTAGCTCTCTGTGGGCCGAAACAAACGCAATGGCCATAGCT	3985	DB	TTTCTTATCCATCTGCG
2584	QY	AGGGCTCTTCTCCAAAAACCCAAAAATTTTATTTGTTGAGTGGCCCACTTCAGCCCTCGAT	2643	QY	TTTCTTATCCATCTGCG
3986	DB	CGTGCCCTTGTGTAGACAGCTCATATTTTGTCTTTTGGTGAAGCCACGTCAGCTCTGAT	4045	DB	TTTCTTATCCATCTGCG
2644	QY	AATGACAGTGAGAGGTGTTCAGATGCGCTTGTATTAAGCCAGGACGGGAAGGACATGC	2703	QY	TTTCTTATCCATCTGCG
4046	DB	ACAGAAGTGAAGGTTGTCCAAAGAGCCCTGGAACAAAGCCAGAGAAGCCGCACTGC	4105	DB	TTTCTTATCCATCTGCG
2704	QY	CTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAACGCAATTTGATGTGTTCTTGCAC	2763	QY	TTTCTTATCCATCTGCG
4106	DB	ATTGTGATTGCTCACCGCTGTCCCAATCCAGATGCAAGTGAATAGTGTGTTTTCAG	4165	DB	TTTCTTATCCATCTGCG
2764	QY	AATGGAAGATTAAGGAAACAAAGGAATCTATCAAGAGCTCTCTGAGAAATCGAGACATAT	2823	QY	TTTCTTATCCATCTGCG
4166	DB	AATGGCAGAGTCAAGGAGCATGGCAGCATCACAGCTGTGSCACAGAAAGGCATCTAT	4225	DB	TTTCTTATCCATCTGCG
2824	QY	TTTTAAGTTAGTAATGCCAGTCAAG	2848	QY	TTTTAAGTTAGTAATGCCAGTCAAG
4226	DB	TTTTCAATGGTCAAGTGTCCAGGCTG	4250	DB	TTTTCAATGGTCAAGTGTCCAGGCTG

RESULT 4

```

1 RECORDING
2 5206352-3
3 ;Patent NO. 5206352
4 ; APPLICANT: Roninson, Igor B.;Pastan Ira H.;Gottesman,
5 ;Michael M.
6 ;
7 ; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
8 ; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
9 ;
10 ; NUMBER OF SEQUENCES: 4
11 ;
12 ; CURRENT APPLICATION DATA:
13 ; APPLICATION NUMBER: US/07/622,836
14 ; FILING DATE: 24-SEP-1990
15 ;
16 ; PRIOR APPLICATION DATA:
17 ; APPLICATION NUMBER: 892,575
18 ; FILING DATE: 01-AUG-1986
19 ; APPLICATION NUMBER: 845,610
20 ; FILING DATE: 28-MAR-1986

```


PRIOR APPLICATION DATA:			Query Match				
APPLICATION NUMBER: DE P 44 31 973.8			36.1%; Score 1030.2; DB 2; Length 6505;				
FILING DATE: 08-SEP-1994			Best Local Similarity 62.2%; Pref. No. 3e-288;				
PRIOR APPLICATION DATA:			Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;				
APPLICATION NUMBER: DE 195 03 952.1							
FILING DATE: 07-FEB-1995							
PRIOR APPLICATION DATA:							
APPLICATION NUMBER: PCT/EP95/03175							
FILING DATE: 10-AUG-1995							
ATTORNEY/AGENT INFORMATION:							
NAME: Berman, Richard J.							
REGISTRATION NUMBER: 39,105							
REFERENCE/DOCKET NUMBER: P1614-7007							
TELECOMMUNICATION INFORMATION:							
TELEPHONE: (202)638-5000							
TELEFAX: (202)638-4810							
INFORMATION FOR SEQ ID NO: 5:							
SEQUENCE CHARACTERISTICS:							
LENGTH: 6505 base pairs							
TYPE: nucleic acid							
STRANDEDNESS: double							
TOPOLOGY: circular							
MOLECULE TYPE: DNA							
US-08-793-610-5							
QY	166	ATTATTGATAGAAACCCAGTATAGTAACCTTTTCCACAGCTGGATATAAACCTGTAATCC	225	QY	826	CGACTTTCTATTTCGAAGTCAGATTGTGACCTTAAGAGATGAATGCTGGCG	885
DB	2918	ATAATTGATAAAGCCAAAGTATTGACAGCTATTTCGAAGAGTGGGCACAAACCCAGATAAT	2977	DB	3578	CGTTTGTCTACAGTTTCGTAATGCTGACGTCGCTGGTTCGATGATGGAGTCATTGTG	3637
QY	226	ATAGAGCACTGGGAATTTAAAAATGTTCTTTTCAATATTCCATCAAGACCATCTATC	285	QY	886	GAGAAAGGAGACATGCTGAACTAATGCGCAACAGAGTCTATATATTCACTTGTGATG	945
DB	2978	ATTAAGGGAATTTGGAATTCAGAAATGTTTCACTTCAGTTTACCCATCTCGAAAGAAAGTT	3037	DB	3638	GAGAAAGGAAATCATGATGAATCATGAAGAGAGAAAGGCAATTTACTTCAAACTTGTCA	3697
QY	286	AAGATCTCGAAGGCTGCAATCTCAGAAATTAAGTCTCGAGAGACAGTCGCTTGGTCGGT	345	QY	946	TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTCTTA	997
DB	3038	AAGATCTTGAAGGCTGCAATCTCAGAAATTAAGTCTCGAGAGACAGTCGCTTGGTCGGT	3097	DB	3698	ATCGACAGCAGAGGAAATGAAGTTGAATTTAGAAATGCGAGCTGATGAATCCAAAGTGAA	3757
QY	346	CTCAATGCGAGTGGGAAGAGTACGGTAGTCAGCTCTTCGAGAGGATATATGATCCGGAT	405	QY	998	-----CTGAAGAAAGACCAACTCTCTCTTGCCTCTGCACTCTGTGAAGAGCATCA	1045
DB	3098	AACAGTGGCTGTGGGAAGAGCACAAACAGTCCAGCTGATGAGAGGCTCTATGACCCACA	3157	DB	3758	ATTGATGCTTGGAAATGCTTCAAAATGATCAAGATCCAGTCTAATAAGAAAAAGATCA	3817
QY	406	GATGGCTTTATCATGTGGATGAGAAATGACATCAGAGCTTTAAATGTCGGCCATTTATCGA	465	QY	1046	-----AGTCAGACTTCAATTGACAGGCTCAGGAATCCACCCAACTCT	1086
DB	3158	GAGGGGATGCTCAGTGTGATGGACAGGATATTAGGACCAATAATGTAAGGTTTCTACGG	3217	DB	3818	ACTCGTAGGAGTGTCCGTGGATCAACAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT	3877
QY	466	GACCAATATTGAGTGGTTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAAACAT	525	QY	1087	AAAGAGATAAGTCTTCTCGAAGTCTCTCTATTAAAAATTTTAAAGTTTAAACAGAGCTGAA	1146
DB	3218	GAAATCATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	3277	DB	3878	CTGGATGAAAGATATACCTCCAGTTTCTTTTGGAGGATATGAAGCTAAATTTAACTGAA	3937
QY	526	ATCAAGTATGACAGAGATGATGTGACTGATGAAGAGATGGAGAGCAGCAGAGGGAAGCA	585	QY	1147	TGSCCTTTTGTGGTCTCTGGGGACATTTGGCTTCTTCTTAAATGGAACCTGTTCATCCAGTA	1206
DB	3278	ATTGCTATGCGCTGGAATGTCAACATGATGAGATGAGATGAGATGAGATGAGATGAGATG	3337	DB	3938	TGSCCTTTTGTGGTCTCTGGGGACATTTGGCTTCTTCTTAAATGGAACCTGTTCATCCAGTA	1266
QY	586	AATGCTATGATTTTATCATGGATTTCTTAATAAATTTAATACATTTGGTGGGGAATAA	645	QY	1207	TTTTCCATCATCTTTGCAAAAATTAACCATGTTTGGAAATTAATGATAAAACCAATTA	1266
DB	3338	AATGCTATGATTTTATCATGGATTTCTTAATAAATTTAATACATTTGGTGGGGAATAA	3397	DB	3998	TTTGAATTAATATTTTCAAGATTTAGGGGTTTTTACAGAAATGATGATCCTGAAACA	4057
QY	646	GGAGTCAATGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	705	QY	1267	AAG---CATGATGACAGAAATTTATCCATGATTTCTGTCATTTGGGGTGTATTGCTTT	1323
DB	3398	GGGGCCCGTTGAGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3457	DB	4058	AAAGGACAGATAGTAATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	4117
QY	706	AACCCCAAGATTTTATGATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	765	QY	1324	GTGAGTTATTTATGACAGGATTTATTTACGCGAGAGAGGGGAAATTTTAAAGATGAGA	1383
DB	3458	AACCCCAAGATTTTATGATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3517	DB	4118	ATTACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	4177
QY	766	GCTGTTTCAAGCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	825	QY	1384	TTAAGGACATCTGCGCTTCAAGCCATGTTTATATCAGGATATTGCTGTTTCTGATGAAAG	1443
DB	3518	GCTGTTTCAAGCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3577	DB	4178	CTCCGATCATGTTTTCGATCCATGCTCAGACAGAGTGTGAGTTGTTGATGACCTT	4237

APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARRIS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Nikaide, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-SEP-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/031175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6

Query Match 36.1%; Score 1030.2; DB 2; Length 9318;
Best Local Similarity 62.2%; Pred. No. 3.7e-288;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
QY 166 ATTATTGATTAAGAACCCAGTATAGATACTTTTCCACAGCTGGATTAACCTGATCC 225
DB 2877 ATAATTGATTAAGAACCCAGTATAGATACTTTTCCACAGCTGGATTAACCTGATCC 2936
QY 226 ATAGAGGAACTGTGGAAATTTAAATAATGTTCTTCAATTATCCATCAAGACCATCTATC 285
DB 2937 ATTAAGGAAATTTGAAATTCAGAAATGTTCACTTCACTTACCATCTCGAAAGAAGTT 2996
QY 286 AAGATTCTGAAAGCTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTGGCTTGGTGGT 345
DB 2997 AAGATCTTGAAGGCTTGAACCTCAAGTGCAGAGTGGGACAGCGTGGCCCTGGTTGA 3056
QY 346 CTCAATGCGAGTGGAGAGTACCGTATGTCAGCTTCTGACAGAGTATATATGATCCGAT 405
DB 3057 AACAGTGGCTGTGGAGAGAGACCAACAGTCCAGTGTATGACAGAGCTCTATGACCCACA 3116
QY 406 GATGGCTTTATCATGCTGGATGAGATGACATCAGAGCTTTTAAATGTGCGGCATTTATCGA 465
DB 3117 GAGGGATGCTCAGTGTGTGATGGACAGGATATTAGGACCAATAATGTAAGTTTCTACGG 3176
QY 466 GACCATATGAGTGGTGTAGTCAAGGCTGTTTTCGGGACCAACCATCAGTAACAT 525
DB 3177 GAAATCATTTGTTGTGTGAGTCAAGAACCTGTTATTTGTTGCCACACAGATAGCTGAAAC 3236

RESULT 6
US-08-793-610-6
; Sequence 6, Application us/08793610
; Patent No. 5858744
; GENERAL INFORMATION:

1564	ATCATTTCTCTTTATATATGGAATGGAGATGACATTTCTGTGATTTCTGATGATTTGCTCCAGTA	1623	TTTATATCTCTTCATCTATGTTGGCAACTAACACATGTTACTCTTAGCAATTTGTACCCTATC
4317			
1624	CTTGCCGTGACAGGAATGATTTGAAACCCGACCAATGCATGGATTTTGGCAACAAAGATAAG	1683	
4377	ATTGCAATAGCAGAGTTGTTGAATGAATGAATGTTTGTCTGGACAAGCACTGGAAGATAAG	4436	
1684	CAAGAACTTAAGCATGCTTGGAAAGATAGCAACTGAAAGCTTTTGGAGNATATAGTACTATA	1743	
4437	AAAGAACTAGAAAGTGTCTGGGAAGATCGCTACTGAAAGCAATAGAAAACTTTCCGAACCGTT	4496	
1744	GTGTCATTTAAACAAGGGAAAAGCCCTTCAGACGAAATGTATGAAGAGATGCTTCAGACTCAA	1803	
4497	GTTCCTTTGACTCAGAGACGCAAGATTTGACACATATGATGTCAGAGTTTGCAGGTACCA	4556	
1804	CACAGAAATATCTCGAAGAAAGACACAGATTTATTTGAGAGCTGTTATGCATTCAGCCATGCC	1863	
4557	TACAGAAACTCTTTGAGGAAAGCAACACATCTTTGGAATTTACATTTTCTTCACCCAGGCA	4616	
1864	TTTATATATTTTCCCTATGACAGCAGGGTTTCGATTTGGAGCCCTATTAAATTCAGCTGGA	1923	
4617	ATGATGTTATTTTCTATGCTCGATGTTTCOGTTTGGAGCCTTACTTTGGTGGCACATAAA	4676	
1924	CGAATGACCCCGAGAGGGCATGTTTCATAGTTTTTACTGCAATTTGCCATATGAGCTATGGCC	1983	
4677	CTCATGAGCTTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTTGTCTTTGGTGGCCATGGCC	4736	
1984	ATCGGAAAAACGCTCGTTTGTGCTCTCTGTAATATTCAAAAGCCAAATTCGGGGGCTGGCCAT	2043	
4737	GTGGGGCAAGTCAGTTCATTTTGTCTCTGACTATGCCAAAGCCAAATATCAGCAGGCCAC	4796	
2044	CTGTTTGCCCTGTGGAAGAAAGAAAACMAATATAGACAGCGGAGTCACAGNAGGGGAAAAAG	2103	
4797	ATCATCATGATCATTTGAAAAAAACCCCTTTGATTTGACGCTACAGCAGGGAAGCCCTAATG	4856	
2104	CCAGACACATGTGAAGGGAATTTAGAGTTTTCGAGAAGTCTCTTTCTTCTATCCATGTCCG	2163	
4857	CCGAACACATTTGGAAGGAATGTCAATTTGTTGAAGTTGTTATTTCAACTATCCACCCGCA	4916	
2164	CCAGATGTTTTCACTCTCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAGACAGTAGCA	2223	
4917	CCGGACATCCCACTGCTTCAGGCACTGAGCCTGGAGTGAAGAAAGGCCACAGACGTGGCT	4976	
2224	TTTGTGGGAGCAGCGCTGTGGGAAAAGCACTTCTGTTCAACTTCTTCGACAGACTTTAT	2283	
4977	CTGTTGGGCGAGCAGTGTGGGAAAGACACAGTGTCCAGCTCTCTGGAGCGGTTCTAC	5036	
2284	GAACCCGTGAAGGACAAAGTCTGTTGATGTTGATGATGCAAGAAAGTAATGAATGTACAG	2343	
5037	GAACCCCTGGCAGGGAAAGTGCTCTGTATGTCGCAAGAAATAAAGCGACTGAATGTTTCAG	5096	
2344	TGCTCCGTTCCCAATAGCAATTCGTTCTCTCAAGAGCTGTGCTCTTTCAACTGCAGCATTT	2403	
5097	TGGCTTCGAGGACACACTGGGSCATCGTGTCCAGAGGCCATCTCTGTTGACTGCAAGATTT	5156	
2404	GCTGAGAAATCGCCTATGGTGAACACAGCCGTGTGGTGCCATTTAGATGAGATCAAGAA	2463	
5157	GCTGAGAAATTCCTATGAGACAACAGCCCGGTGTGTACAGGAAGAGATCGTAGG	5216	
2464	GCCGCAATTCGAGCAAAATATCCAATCTTTTATTTGAAGGTTCTCCCTGAGAAATACAAACA	2523	
5217	GCAGCAAGAGGCCCAACATACATGCTCTCATCGAGTCACTGCTCTAATAATATAGCACT	5276	
2524	CAAGTTGGACTGAAGGAGCAGACTTTCTGGGGGCCAGAAACAAGACTAGCTATTGCA	2583	
5277	AAAGTAGGACAAAGGAACTCAGCTCTCTGGTGGCCAGAAAAACCGCATTTGCCATAGCT	5336	
2584	AGGGCTCTTCTCCAAAAACCCAAAAATTTTATTTGATGAGGCGCACTTCAGCCCTCGAT	2643	
5337	CGTGCCCTCTGTAGACAGCTCATATTTTGTCTTTTGGATGAAGCCCACTCAGCTCTGGAT	5396	
2644			

Db	5397	ACAGAAAGTGAAGGTTGTCCAGAGAGCCTCGACAAAGCCAGAGAGGCCGCACTGC	5456
Qy	2704	CTAGTGGTCTACTCAGAGGCTCTCTGCAATTACAGACGCAGATTTGATGTGTTGCAC	2763
Db	5457	AATTGTATTGCTCAGCGCCTGTCCACCATCCAGAATGCAGACTTAATAGTGGTGTTCAG	5516
Qy	2764	AATGGAAGAGATAAGGAAACAAAGCACTCATCAAGAGCTCTCTGAGAAATCGAGACATAT	2823
Db	5517	AATGGCAGAGTCAAGGAGCATGCAAGCATCAGCAGCTGTCGCACAGAAAGCATCTAT	5576
Qy	2824	TTTAAAGTTAGTGAATGCACAGTCAG	2848
Db	5577	TTTTCAATGGTCAGTGTCCAGGCTG	5601

RESULT 7

US-08-784-649A-1
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sikic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/784,649A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: Reg.No. 5830697 36,677
; REFERENCE/DOCKET NUMBER: 06037/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4264 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-784-649A-1

	Query Match	36.0%	Score 1028.6	DB 2	Length 4264
	Best Local Similarity	62.2%	Pred. M. 6.9e-288		
	Matches 1894	Conservative	0	Mismatches 989	Indels 42
				Gaps 3	
Qy	156	ATTATTGTATGAACACCAGATAGATAACATTTTCCACGCTGCGATATAAACCTGAATCC	225		
Db	1240	ATAATTGTATATAAGCCCAAGTATTGACAGCTATTTCGAAGAGTGGGCACAAACCGAGTAAT	1299		
Qy	226	ATAGAAGCAACTGTGTGAATTTTAAATAATCTTTCTTTCAATTATTCATCAAGAGCCATCTATC	285		
Db	1300	ATTAAGGGAAATTGGGAATTCAGAAATCTTCACITTCAGTTACCATCTCGAAGAAAGATT	1359		
Qy	286	AAGATCTGAAAGGTCTGAATCTCAGAATTAAGTCTGGAGAGACAGTCGCCTTCGTCGGT	345		
Db	1360	AAGATCTTGAAGGGCTCGAATCTCAAGGTGCAGAGTGGGAGAGCGTGGCCCTCGTTTGA	1419		

QY 1384 TTAAGACACTTGGGCTTCAAGCCGANGTTATATCAGGATATGCTGCTGTTGATGAAAG 1443
Db 2500 CTCGATACATGGTTTCGGATCCATGCTCAGACAGGATGTGAGTTGGTTGATGACCT 2559
QY 1444 GAAACACGACAGAGGCTTGCACACATATATAGCCATAGATATAGCACAAATTCAGGA 1503
Db 2560 AAAACACCATGAGCAATGACATACAGGCTCGCCATGATGCTGCTCAGTTTAAAGG 2619
QY 1504 GCAACAGTTCCAGGATGGCTCTTAACACAAATGCAACTAAATGAGGACTTTCAGTT 1563
Db 2620 GCTATAGTTCCAGGCTTGTGTAATACCCAGAAATATAGCAAACTCTGGACAGGAATA 2679
QY 1564 ATCATTTCTTTATATATGATGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1623
Db 2680 ATTATATCTTCACTATGTTGGCACTAACACTGTTACTCTTACGAAATGTTACCCATC 2739
QY 1624 CTTCCGCTGACAGGAATGTTGAAACCGCAATGATGATGATGATGATGATGATGATGAT 1683
Db 2740 ATTGCAATAGCAGGATGTTGTAATGAAATGATGTTGTTGCAACAGCACTGAAAGATAAG 2799
QY 1684 CAAGAACTTAGCATCTGGAAGATGACCACTGATGATGATGATGATGATGATGATGATGAT 1743
Db 2800 AAGAAGCTTAGAAGGTTGTTGGAAGATGCTACTGAAGCAATAGAAATCTCCGAACCGTT 2859
QY 1744 GTGTCAATTAACAAGGGAAGGCTTCCAGCAAAATGATGAAGAGATGCTTCAAGCTCAA 1803
Db 2860 GTTCTTTGACTCAGGACGAGAGTTTGAAATATATGATGATGATGATGATGATGATGAT 2919
QY 1804 CACAGAAATCTCGAAGAAAGCAGATATATGAGAGCTGTTATGATGATGATGATGATGAT 1863
Db 2920 TACAGAAATCTTTGAGGAAAGCAGATATATGAGAGCTGTTATGATGATGATGATGATGAT 2979
QY 1864 TTTATATATTTGCTATGACAGGAGTTTCGATTTGAGCTTATTTAAATCAAGCTGGA 1923
Db 2980 ATGATGATTTTCTATGCTGATGTTTCGGTTTGGAGCTTACTTGGTGGACATATAA 3039
QY 1924 CGATGACCCAGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
Db 3040 CTCATGAGTTTGGAGATGTTCTGTTAGTATTTTCACTGTTGTTGTTGTTGTTGTTGTT 3099
QY 1984 ATCGGAAAGACGCTGTTTGGCTCTCGAATATTTCCAAAGCAATCGGGGCTGCGCAT 2043
Db 3100 GTGGGCAAGCTCAGTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3159
QY 2044 CTGTTTGGCTTTTGGAAAGAAACCAATATGACAGCCGCTGAGGAGGAGGAAAG 2103
Db 3160 ATCATCATGATCAATGAAAGAAACCCCTTGTATGACAGCTACAGCAGGAGGCTTATG 3219
QY 2104 CCAGACATCTGAGGGAATTTAGAGTTTCGAGAGCTCTTCTTCTTCTTCTTCTTCTTCT 2163
Db 3220 CCGAACATTTGGAGGAATTTGACATTTGGTGAAGTTGTTTCACTATCCACCCGA 3279
QY 2164 CCAGATGTTTTCATCTCCGCTGCTTATCCCTCAGTATTTGAGCGAGGAAGACAGTAGCA 2223
Db 3280 CCGGACATCCAGTGTCTTCAAGGACTGAGCTGAGGCTGAGGAGGAGGAGGAGGAGGAG 3339
QY 2224 TTTGTTGGGAGCAGGCTGTTGGAAAGCACTTCTGTTCACTTCTGAGAGCTTAT 2283
Db 3340 CTGTGTTGGCAGCAGTGGCTGTTGGGAGAGCAGTGTCCAGCTCTTGGAGCGGTTCTAC 3399
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Db 3460 TGGCTCCGAGCAGCCTTGGGATCGTTCCAGGAGGCCATCTCTTGTGACTGAGCAAT 3519
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QY 2464 GCGCAATGAGCAAAATATCCATTTCTTTTATGAGGTTCTTCTGAGGATGATGATGATGAT 2523

Db 3580 GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3639
QY 2524 CAAATTTGGGACTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2583
Db 3640 AAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3699
QY 2584 AGGCTTCTTCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2643
Db 3700 CGTGGCTTCTTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3759
QY 2644 AATGACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2703
Db 3760 AAGAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3819
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Db 3820 ATTGTGATTTCTCAGCGCTGTCCACCATCCAGATCCAGATCTTAATAGTGTGTTTCAG 3879
QY 2764 AATGGAAGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2823
Db 3880 AATGCGAGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2883
QY 2824 TTTAAGTTAGTGAATCAGAGTCAAG 2848
Db 3940 TTTTCAATGCTCAGTGTCCAGGCTG 3964

RESULT 8
US-08-784-649A-5
; Sequence 5, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sixic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,649A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: Reg.No. 5830697 36,677
; REFERENCE/DOCKET NUMBER: 06037/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4264 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-784-649A-5

Query Match 36.0%; Score 1028.6; DB 2; Length 4264;
Best Local Similarity 62.2%; Pred. No. 6.9e-288;
Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

166 ATATTGATGAAGAACCCAGTATAGATAACTTTTCCACAGCTCGATATACACCTGATCC 225
1240 ATAAATGATTAAGCCCAAGTATTCACAGCTATTTGGAAGAGTGGGCAAAACAGATAT 1299
226 ATAGAAGGAACGTGGAAATTTAAATATTTCTTTCAATTTATCCATCAAGACCATATC 285
1300 ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAAGAGTT 1359
286 AAGATTCGAAAGGTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTCGCTTGGTGGT 345
1360 AAGATCTTGAAGGCCCTGAACCTGAAGGTGAGAGTGGGAGAGCGTGGCCCTGGTTGGA 1419
346 CTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTTCTGAGAGGTTTATATGATCCGGAT 405
1420 AACAGTGGCTGTGGAAGAGCACAACAGTCCAGCTGATGAGAGGCTCTATGACCCACA 1479
406 GATGGCTTTATCATGGTGGATGAGATGACATCAGAGCTTTAATGTGGGCAATTATCGA 465
1480 GAGGGAGTGTGAGTGTGATGAGCAGATATTAGGACCAATAAATGTAAGGTCTTACGG 1539
466 GACCATAATGAGTGGTGTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAT 525
1540 GAATCATTTGGTGTGGTGTGAGTCAAGAGCTGTATTGTTGCCACCATGATGGAAC 1599
526 ATCAAGTATGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
1600 ATTGCTATGCGGCTGGAATGTCAACATGATGATGATGATGATGATGATGATGATGAT 1659
586 AATGCGTATGATTTATCATGAGTGTTCCTAAATAATTTAATACATTTGATGAGGAA 645
1660 AATGCGTATGATTTATCATGAGTGTTCCTAAATAATTTAATACATTTGATGAGGAA 1719
646 GGAGCTCAATGATGAGTGGAGGAGCAAGAGGATGCAATTTGCTGCTGCTTGTAGTGA 705
1720 GGGGCCAGTTGAGTGGGAGAGCAGAGGATGCGCATTTGACAGCTGCGCTGCTGCTG 1779
706 AACCAGAGATTCGATTTAGTGGCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
1780 AACCAGAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1839
766 GCTGTTCAAGCTGACATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
1840 GTGGTTCAGGTGGCTCTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1899
826 CGACTTTCTACTATTGAGAGTGCAGATTTGATTTGAGGAGGAGGAGGAGGAGGAGGAG 885
1900 CGTTTGTCTACGTTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1959
886 GAGAAAGAGCAGATGCTGAACTAATGCGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
1960 GAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2019
946 TCACAGGATATTAAGAAAGCTGATGAACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 997
2020 ATGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2079
998 -----CTGAAGAAAGAGCAACTTCCTCTGCACTCTGCAAGAGGAGGAGGAGGAG 1045
2080 ATTGATGCTTGGAAATGCTTCAATGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2139
1046 -----AGTCAGATTCATTGCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1086
2140 ACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2199
1087 AAGAGATAGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1146
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2260 TGGCCTTTTGTGGTCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2319

1207 TTTTCCATCATCTTTGCAAAAATTTATACCACTGTTTGGAAATAATGATATAAACCAATTA 1266
2320 TTTGCAATATATTTTCAAGATTTATAGGGTTTTCAGAAATTCATGATGATGATGATGAT 2379
1267 AAG---CATGATGAGAGAAATTTATCCATGATATTCGTCAATTTTGGGTGTTATTTGCTTT 1323
2380 AAAACGACAGATAGTAACCTTTTTCACATATTTTCTAGCCCTTGGAAATTTATTTCTTTT 2439
1324 GTCAGTTATTTTCATGAGGATTTATTTACGCGACAGCAGGAGGAAATTTTAAACGATGAGA 1383
2440 ATTACATTTTCTTTCAGGGTTTCATTTGGCAAGCTGGAGAGATCCTCACCAGGCG 2499
1384 TTAAGACATCTGGCCTTCAAGCCATGTTATATCAGGATATTTCCCTGGTGTGATGAAAG 1443
2500 CTCGATACATGTTTTCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGTATGACCCCT 2559
1444 GAAAACAGCAGCAGGAGGCTTTGACAAATATTAGCCATAGATATATGACAAATTTCAAGGA 1503
2560 AAAAAACACCTGAGCATTTGACTACAGGCTGCGCAATGATGCTGCTCAAGTTAAAGG 2619
1504 GCAACAGGTTCCAGGATGGCGTCTTAAACAAAATGCAAAATGCAAAATGGGACTTTTCAATT 1563
2620 GCTATAGGTTCCAGGCTGCTGTAATTAACCCAGATATAGCAAAATCTTGGACAGGAATA 2679
1564 ATCATTTCTTTATATATGATGGAGATGACATCTCTGATTTCTGAGTATTTGCTCCAGTA 1623
2680 ATTATATCTTCTCATCTATGTTGGCAACTTAACATCTTTACTCTTAGCAATTTGATCCATC 2739
1624 CTTCGCGTGCACAGGATGATTTGAAACCGCAGCAATGACTGGATTTTCCCAACAAAGATAAG 1683
2740 ATTGCAATAGCAGGAGTGTGTTGAAATGAAATGTTGTTCTGGAACAACACTGAAAGATAAG 2799
1684 CAAGAACTTAAGATGCTGGAAGATAGCACTGAAGCTTTGGAGATATATGATCTATA 1743
2800 AAGAACTAAGAGGTTGCGGAAGATGCTACTGAAGCAATAGAAATCTTCGAAACCGTT 2859
1744 GTGCTAATAACAGGAGGAAAGCCTTCGAGCAAAATGATGAAGAGATGCTTCAGACTCAA 1803
2860 GTTCTTTGACTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGSTACCA 2919
1804 CACAGAAATACCTCGAAGAAAGCAAGATTAATGGAAGCTGTTATGCAATTCAGGCTATGCC 1863
2920 TACAGAACTCTTTGAGGAAAGCACAATCTTTGGAATTTACATTTTCTTCCATCCAGGCA 2979
1864 TTTATATATTTTCTGCTATGACAGGCTTTTCAGTTTGGAGCTTATTTAATTTCAAGCTGGA 1923
2980 ATGATGATTTTCTTCTGCTGATGTTTCCGTTTGGAGCTTACTTGTGTGGCACAATAA 3039
1924 CGAATGACCCCGAGAGGCAATGTTCAATGATTTTATGCAATTTGCAATGAGCTATGGCC 1983
3040 CTCATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAGCTGTTGCTCTTTGCTGCTATGGCC 3099
1984 ATCGGAAACCGCTCGTTTGGCTCTGATATTTCCAAAGCCAAATCGGGGCTGCGCAT 2043
3100 GTGGGCAAGTCAGTTCAATTTGCTCTGCTGATGCTGCAAGGCAAAATATCAGAGCCAC 3159
2044 CTGTTTGCCTTTGTTGAAAAGAAACCAATATAGACAGCGCAGCTCAAGAAAGGAAAG 2103
3160 ATCATCATGATCATTTGAAAACCCCTTTTGAATGACAGCTACAGCACGGAAGGCTTAATG 3219
2104 CAGACACATGTAAGGGAATTTAGGTTTTCAGAGTCTCTTCTTCTTCTTCTTCTTCTTCTT 2163
3220 CCGAACATTTGGAAGGAAATGTCATTTGTTGAGGTTGTTATTTCAACTATTTCCACCCGA 3279
2164 CAGATGTTTCTCATCTCTCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAAGCAGTAGCA 2223
3280 CCGGACATCCAGTGTCTTCAGGGAATGAGCTGAGGAGTGAAGAGGCGCAGAGCTGGCT 3339
2224 TTTTGGGAGCAGCGGCTGTGGGAAAGACATTTCTGTTCAACTTCTGAGAGACTTTAT 2283
3340 CTGGTGGGAGCAGTGGCTGTGGGAGAGCAGATGCTGCTGAGGAGGTTCTAC 3399
2284 GACCCCGTCAAGGACAAGTGTCTGTTGATGTTGATGCTGGAAGCAAAAGATTTGAATGTACAG 2343

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RESULT 9
US-09-306-417-2
; Sequence 2, Application US/09306417
; Patent No. 6548301
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral Gene Transfer Vectors
; FILE REFERENCE: P50491
; CURRENT APPLICATION NUMBER: US/09/306,417
; CURRENT FILING DATE: 1999-05-06
; EARLIER APPLICATION NUMBER: DE 198 22 115
; EARLIER FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proviral
; OTHER INFORMATION: plasmid DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(8630)
; OTHER INFORMATION: retroviral expression vector SPbeta91mSA1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(160)
; OTHER INFORMATION: plasmid backbone (pUC)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (161)..(677)
; OTHER INFORMATION: 5'-LTR

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466	QY	GACCATATTGGAGTGGTTAGTCAAGAGCGCTGTTTGTTCGGACCAACATCAAGTAACT	525
2621	Db	GAAATCATTTGGTGTGGTGTGAGTCAGGAACCTGTATTGTTTGCACCACGATAGCTGAAAC	2680
526	QY	ATCAAGTATGGACGAGATGATGTGACTGNTGAAGAGATGGAGAGAGCGACRAAGGAGACA	585
2681	Db	ATTTCGTATGCGCGTGAAATGTCAACATGGATGAGATTGAGAAAGCTGTCAAGNAGCC	2740
586	QY	AATGCGTATGATTTTATCATTGGAGTTTCTTAATAAATTTAAATACATTTGGTAGGGAAAAA	645
2741	Db	AATGCCATATGACTTTATCATGAAACTGCCCTCTAAATTTGACACCGCTGGTTGGAGAGAGA	2800
646	QY	GGAGCTCAAAATCAGTGGAGGCGAGAAAACAGAGGATCGCAATTTGCTCGTCCCTTAGTTCCA	705
2801	Db	GGGGCCAGTTGAGTGGTGGGCAAGAAGAGAGATCGCCATTGCACTGCTCCCTGGTTCCG	2860
706	QY	AACCCCAAGATTCGATTTTATGATAGGCTAGCTGCTGCCCTGGATTTCAGAAAGCAAGTCA	765
2861	Db	AACCCCAAGATTCCTCTGCTGATGAGGCCACGTGAGCCTTCGACACAGAAAGCGAAGCA	2920
766	QY	GCTGTTTCAAGCTGCATCTGAGAAAGCGAGCAAAAGCTCGGACTACAAATCGTGGTAGCACAC	825
2921	Db	GTGGTTTCAGGTGCGCTCTGCAATAAGGCCAGAAAAGGTCGGACCAACATTTGTGATAGTCAAT	2980
826	QY	CGACTTTCTACTATTTCGAAGTCGAGATTTGATTGTGACCTTAAAGGATGGAAATGCTGGCG	885
2981	Db	CGTTTGCTACAGTTTCGTAAATGCTGACGTCATCGCTGGTTTCGATGAGAGAGTCAATTGTG	3040
886	QY	GAGAAAGGAGCAATGCTGAACTTAATGGCAAAACGAGGTCCTATATTATTTCATCTTGTGATG	945
3041	Db	GAGAAAGGAAATCATGATGAATCTCAATGAAGAAAGGCAATTTACTTCAAACTTGTTCACA	3100

Qy	946	TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATATGACATATTCTA	----- 997
Db	3101	ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAATGCAGCTGATGAATCCAAAAGTGAA	3160
Qy	998	-----CTGAAAGAAAGCAGCAACTCACTTCTCTCGCACTCTGTGAAGAGCATCA	--- 1045
Db	3161	ATTGATGCCCTTGGAAATGTCTTCAATGATTCAGATCCAGTCTTAATAGAAAGAAAGTCA	3220
Qy	1046	-----AGTCAGACTTCATTGAACAAGGCTGAGSMAATCCACCCAAATCT	1086
Db	3221	ACTCGTAGGAGTGTCCGTGGATCACAAGCCACAGACAGAAAGCTTAGTACCAAGAGGCT	3280
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Db	3281	CTGATGAAGTATACCTCCAGTTTCTTTGGAGGATTAAGCTTAAATTTTAACTGAA	3340
Qy	1147	TGSCCTTTTGTGTTCTGGGACATTTGGCTTTCTTTCTAAATGGAACGTGTCATCCAGTA	1206
Db	3341	TGSCCTTAATTTGTGTGTGTTATTTGTGCCATTAATAATGGAGCCTGCAACAGCA	3400
Qy	1207	TTTTCCATCATCTTTGCAAAAATTTATAACCATGTTTGGAAATATGATAAAACCATTA	1266
Db	3401	TTTGCAATATAATTTTCAAGATTTATAGGGGTTTTTACAGAATGATGATCTGTAACA	3460
Qy	1267	AAG---CATGATGCAGAAAATTATTCATGATATTCGTCAATTTGGGTGTATTGTGCTT	1323
Db	3461	AAGCAGAGATAGTACTGTTTCTACTATTGTTCTAGCCCTTGGAAATATTCTTTT	3520
Qy	1324	GTCAATTATTTTCAGAGGATTAATTTTACGACAGCAGGGGAAATTTTAAAGATGAGA	1383
Db	3521	ATTACATTTTCTTCAAGCTTTCACATTTGGCAAGCTGAGAGATCTTCACCAAGCGG	3580
Qy	1384	TTAAGACACTTGGCTTCAAGCCATGTTATATCAGGATATGCTCTGTTTGATGAAAG	1443
Db	3581	CTCCGATACATGTTTTCCGATCCATGCTCAGACAGGATGTAGTTGGTTTGATGCCCT	3640
Qy	1444	GAAAAACAGCAGGAGCTTGAACAATATTAGCCATAGATATAGCACAAATTCAGAEGA	1503
Db	3641	AAAAACACCACTGGAGCATTGACTACACAGGCTGCCAATGATGCTCTCAAGTTAAAGGG	3700
Qy	1504	GCAACGGTTCAGGATGGCGTCTTAACACAAATCGCACTACACTGAGGACITTCAGTT	1563
Db	3701	GCTATAGTTCCAGGCTGTCTGTANTTACCAGATATAGCAATCTTGGGACAGGAATA	3760
Qy	1564	ATCATTTCCCTTTATATGATGGATGGAGATGACATTCCTGATTCGAGTATTGCTCCA	1623
Db	3761	ATTATATCCTTCTATATGTTGSCAACTAACACTGTTACTCTTAGCAATTGTACCCATC	3820
Qy	1624	CTTGCCGTGACAGGAATGATTGAACCGCAGCAATGACTGGATTTGCCAACAAAGATAAG	1683
Db	3821	ATTGCAATAGCAGAGTTGTGTAAGTGAANAATGTTGTCTGGCAAGCACTGGAAGATAAG	3880
Qy	1684	CAAGAACTTAAGCATGCTCGAAAGATAGCAACTGAAGCTTTGGAGAATATACGTACTATA	1743
Db	3881	AAAGAACTAGAGGTGCTGGGAGATGCTTACTAGAGCAATAGAAACTTCGGAACCGTT	3940
Qy	1744	GTGTCAATTAACAGGGAAAAAGCCCTTCAGCAATATGATGAGAGATGCTTCAGACTCAA	1803
Db	3941	GTTTCTTTGATCTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCA	4000
Qy	1804	CACAGAAATACCTCGAAGAAGCAGATATTGGAAGCTGTTATGATTTCAGCCATGCC	1863
Db	4001	TACAGAACTCTTTGAGAAAGCACAATCTTTGGAAATTAATTTTCTTCAACCCAGGCA	4060
Qy	1864	TTTATATATTTTGCTATGACAGAGGTTTCGATTTGGAGCCTATTTAATTCAGCTGGA	1923
Db	4061	ATGATGTATTTTCTATGTCTGGAATGTTTCGGTTTGGAGCCTACTTGGTGGCACATAAA	4120
Qy	1924	CGAATGACCCAGAGGCATGTTTCATAGTTTTTACTCAATTCGATATGAGGTATGGGCC	1983
Db	4121	CTCATGAGCTTTGAGGAATGTTCTGTTAGTATTTTCAGCTGTGTGCTTTGGTGCCATGCC	4180
Qy	1984	ATCGAAAAAGCGCTCGTTTTGGCTTCTGAAATATTCAAAGCAATCGGGCGCTGGCAT	2043

4181	DB	GTGGGCAAGTCAGTTCA	TTTGTCTCTGACTATG	CCAAAGCCAAATATAC	GAGCCCAAAATATAC	GAGCCCA	4240
2044	QY	CTGTTTGCCCTGTGTG	AAAGAAACC	CAAAATATAG	CACAGCGCAGTCA	AGAGGAAAG	2103
4241	DB	ATCATCATGATCAT	TGA	AAACCCCTTTG	ATGACAGCTAC	GACGACGAGACCTTAATG	4300
2104	QY	CCAGACACATGTGA	AGGAAATTAGAG	TTTCGAGAAATCTCT	TTTCTTCTTATCATCATGTCCG	2163	
4301	DB	CCGAAACACATCGA	AGAAATGACAF	TTGGTGAAGTTGTAT	TCAACTATCCACCCGA	4360	
2164	QY	CCAGATGTTTTCAT	CTCCGTGGCTTAT	CCCTCAGTATT	GAGCCAGGAAAGACAGTAGCA	2223	
4361	DB	CCGACATCCAGTGT	CTTACGGACTGAC	CTGGAGTGA	AGAGGCCAGACGCTGGCT	4420	
2224	QY	TTTGTGGGAGACAG	CGGCTGTGGGAAAG	ACACTTCTGTGTTCA	ACTTCTTCGACAGACTTTAT	2283	
4421	DB	CTGTTGGGACAG	TGGCTGTGGGAA	GACACAGTGGTCC	AGCTCTCTGGAGCGGTTCTAC	4480	
2284	QY	GACCCGTGCAAGGA	CAAGTCTGTTTGAT	GGTGTGCATGCA	AAAGAAATTTGAATGTACAG	2343	
4481	DB	GACCCCTTGGCAGG	GAAGTCTGCTGTAT	GGCAAGAAAT	AAAGCGACTGAATGTTTCA	4540	
2344	QY	TGCTCGTTTCCAA	ATAGAAATCGT	TCTCAAGACCTGTG	CTTCTTAACTCGACGATT	2403	
4541	DB	TGCTCCGAGCA	CACCTGGGATCGT	GTGCCAGGACCAT	CTCTGTTGACTGCAGCATT	4600	
2404	QY	GCTGAGAA	CATCGCTATGCTG	ACAAACAGCCGTGTG	CTCAATAGATGAGATCA	2463	
4601	DB	GCTGAGAA	CATTGGCTATGG	AGAACACACGCGGTGGT	CTCACAGAGAGATCGTGAGG	4660	
2464	QY	GCGCAAAATGCA	AGCAATATCAT	TTCTTTTATTTGA	AGGCTCTCCTCGAGAAATACACACA	2523	
4661	DB	GCAGCAAGGAG	GCCAACATATG	CTTTCATGCTCTCAT	GAGTCACTGCTTAATAANTATAGCACT	4720	
2524	QY	CAAGTTGGA	CTGAAGGACACAG	CTTCTCGCGGCAGAA	CAAAAGACTAGCTATTGCA	2583	
4721	DB	AAAGTAGAG	AGACAAAGGAACT	CAGCTCTCTGTGG	CGCAGAACACGCACTGSCCATAGCT	4780	
2584	QY	AGGGCTCTTCTC	CAAAAACCCAAATTTTAT	TGTGGATGAGG	CCACTTCAGGCCCTCGAT	2643	
4781	DB	CGTGCCCTTGT	TAGACAGCCTCATAT	TTTGTCTTTTGAT	GAAAGCCAGTCTCGGAT	4840	
2644	QY	AATGACAGT	GAGAGGTGTCTAG	CATGCTTGAT	TAAAGCCAGGACGGCAAGGACATGC	2703	
4841	DB	ACGAAGT	GAAAGTTGTCC	AGAGCCCTG	GCACAAAGCCAGAGAGGCGCCACCTGC	4900	
2704	QY	CTAGTGGT	CACACAGGCTCTCTG	CAATTCAGAACG	CGCAGATTGTGATGTGGTTTGCAC	2763	
4901	DB	ATTGTGAT	TGCTCACCGCCTCTCC	ACCATCCGAATG	CGACACTTAATAGTGGTGTTCAG	4960	
2764	QY	AATGGAAG	AATGAAGAACAG	AGNACTCAT	CAAGACTCTCTGAGAAATCGACATATAT	2823	
4961	DB	AATGGCAG	AGTCAAGGACAT	TGGACGCA	TACGAGCTGCTGGCACAGAAAGCATCTAT	5020	
2824	QY	TTTAAGTTAG	TGAATGCA	CAGTCA	G	2848	
5021	DB	TTTTCAAT	GTGAGTGTCC	AGGCTG		5045	

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RESULT 10
US-09-023-655-1168
; Sequence 1168, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

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Query Match	36.0%	Score 1027.2	DB 4	Length 3924
Best local Similarity	61.9%	Pred. No. 1.7e-287		
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QY	166	ATTATTGATTAAGAAACCCAGATATAGATAA	CTTTTCCACAGCTGGATATATAACCTGAAATCC	225
DB	1140	ATTATTGATTAATAATCTTAAATTTGACAGT	TTTTTCAGAGAGGACACAAACACAGACAGC	1199
QY	226	ATAGAGGAACCTGTGGAAATTTAAAAATGTT	TCTTCAATTTCCATCAAGACCAATCTATC	285
DB	1200	ATCAAAAGGGAATTGGAGTTTCAATGATGTT	CTCATCTTTCTTACCCCTTCGAGAGTAAAGTC	1259
QY	286	AAGATTTCTGAAAGGTCTGAAATCTCAGAA	TTAAAGTCTCGAGAGACAGTCGCTTGGTCCGT	345
DB	1260	AAGATCTTGAAGGSCCTCAACCTGAAGGT	GCAGAGTGGCAGAGCGTGGCCCTGGTTGGA	1319
QY	346	CTCAATGGCAGTGGGAAGAGTACGGTAGTC	CCAGCTTCTGCAGAGAGTTATATGATCCGAT	405
DB	1320	AGTAGTGGCTGTGGGAAGAGACCAACCGT	CCAGCTGATACAGAGGCTCTATGACCCCTGAT	1379
QY	406	GATGGCTTTTATCATGTGTGGATGAGATGA	TCATCAGAGCTTTTAAATGTGGCGATTATCGA	465
DB	1380	GAGGGCACAAATTAACATTGATGGCAGGA	TATTAGGAACTTTAATGTAAACTATCTGAGG	1439
QY	466	GACCATATTGGAGTGGTTAGTCAAGAGCCT	GTGTTTTGTTTCGGGACCAACATCAGTAACAAT	525
DB	1440	GAATAATCAATGGTGTGTGTGAGTCAGGAG	CCCGTGCTGTTTTCCACCAAAATTGCTGAAAAAT	1499
QY	526	ATCAAGTATTCGACAGAGATGATGTGACT	GTGATGAGAGATGGAGAGAGCAGCAAGGGAACGA	585
DB	1500	ATTGTTATGCGCGTGGAAATGTAAACCAT	GGATGAGATAAAGAAGCTGTCAAGAGGCC	1559
QY	586	AATGCGTATGATTTTATCATGGAGGTTTCC	TATATAAATTTAATTCATTTGGTAGGGGAAAAA	645
DB	1560	AACGCCCTATCAGTTTATTCATGAAATTA	CCACAGAAATTTGACACCCCTGGTGGAGAGAGA	1619
QY	646	GGAGCTCAAAATGAGTGGAGGCGCAAAAC	ACAGAGGATCGCAATTGCTCTGTCCTTAGTTTCTGA	705

Db 2700 GAAGCTGCTGGAAGATTGCAACAGAGGCAATAGAAAATATTAGGACAGTTGTGCTTTG 2759
 Qy 1753 ACAGGGAAAAAGCCTTCGAGCAATGATGAAGAGATGCTCAGACTCAACAGAAAT 1812
 Db 2760 ACCAGGAAGAAAATTTGAATCAATGATGTTGAATAATTTGATGACCTTTACAGGAAT 2819
 Qy 1813 ACCTGAAAGAACACAGATTTATGGAAGCTGTTATGCAATTCAGCCATGCCCTTTATATAT 1872
 Db 2820 TCTGTGCAGAGGACACATCTATGNAATTTACTTTTAGTATCTCACAAGCAATTTAGTAT 2879
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 Qy 1933 CCAGAGGCGATGTTCAATAGTTTCTGCAATTCGATATGAGCTATGGCATGCCATCGAAAA 1992
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 Qy 1993 ACCTCGTTTGTGCTCTGCAATTCCTAAAGCCAAATTCGAGGCTCGCATCTGTTTGGC 2052
 Db 3000 GCCAGTTCTATTTGCTCCAGACTATGCTAAAGCTGAAGCTGCTGCAGCCCACTATTCTG 3059
 Qy 2053 TTCTTGAAGAAAGAAACCAATATAGACAGCGGAGTCAAGAGGGAAGGCAAGCCACACA 2112
 Db 3060 CTGTTTGAAGACAACCTCTGATGACAGCTACAGTGAAGAGGGGCTGAAGCTGTATAA 3119
 Qy 2113 TGTGAAGGGAATTTAGAGTTTCGAGAGTCTCTTCTTCTATCCATGTCGCCACATGTT 2172
 Db 3120 TTTGAAGGAATATAACATTTAATGAATGCTGTTCAACTATCCACCCGAGCAACGTTG 3179
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 Qy 2233 AGCAGCGGCTGTGGAAAGCACTCTGTTTCACTTCTGAGAGACTTTTATGACCCCTG 2292
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 Db 3420 ATTGCTATGAGACAAACAGCCGGTTGATCACAGGATGAAATGTGAGTGCAGCAAA 3479
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 Qy 2593 CTCGAAAACCCAAAATTTTATTTGTTGATGAGGCCACTTCAGCCCTCGATATGACAGT 2652
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 Db 3720 GCTCAGCCCTGTCCACCATCCAGATGAGACTTAATAGTGTGTTTTCAGAAATGGAGA 3779
 Qy 2773 ATAAAGGACAGGAACTCATCAGAGCTCTCAGAGAAATCAGAGCATATTTTAAGTTA 2832
 Db 3780 GTCAGAGGAGTGGCAGGCTCAGAGCTGCTGGCACAGAAAGGCAATCTATTTCATATG 3839

Qy 2833 GTGAATGCACAGTCAAGT 2850
 Db 3840 GTCAGTGTCCAGGCTGG 3857
 RESULT 11
 US-09-762-195-2
 ; Sequence 2, Application US/09762195
 ; Patent No. 6677319
 ; GENERAL INFORMATION:
 ; APPLICANT: Stremler, Wolfgang
 ; TITLE OF INVENTION: Phosphatidylcholine as Medication with
 ; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
 ; FILE REFERENCE: 34691/208520
 ; CURRENT APPLICATION NUMBER: US/09/762,195
 ; CURRENT FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: PCT/EP99/02426
 ; PRIOR FILING DATE: 1999-08-06
 ; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
 ; PRIOR FILING DATE: 1998-08-06
 ; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
 ; PRIOR FILING DATE: 1998-12-15
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 3924
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-762-195-2
 Query Match 36.0%; Score 1027.2; DB 4; Length 3924;
 Best Local Similarity 61.9%; Pred. No. 1.7e-287;
 Matches 1682; Conservative 0; Mismatches 1003; Indels 33; Gaps 2;
 Qy 166 ATTATGTATGAAGAACCCAGTATAGATAACTTTCCACAGCTGGATATATAAACCCTGAATCC 225
 Db 1140 ATTATGTATGAAT 1199
 Qy 226 ATAGAAGGAATCTGGAATTTAAATAATGTTCTTTCAATATTCATCAAGACCATCTATC 285
 Db 1209 ATCAAAGGAATTTGGAGTTCAATGATGTTTACATTTTCTTACCTTTCTCGAGCTAACGTC 1259
 Qy 286 AAGATCTGAAAGGCTGAAATCTGAAATTAAGTCTGGAGAGACAGTCCCTTGTGCTGGT 345
 Db 1260 AAGATCTTGAAGGGCTCAACCTGAAGGTGAGAGTGGGAGAGCGTGGCTGGTGGGA 1319
 Qy 346 CTCATGTCAGTGGAGAGTACCGTAGTCTGAGAGTCTGAGAGGTTATATGATCCGGAT 405
 Db 1320 AGTAGTGTCTGGAGAGGACACACCGTCCAGCTGATACAGAGGCTCTATGACCTGAT 1379
 Qy 406 GATGCTTTTATCATGTTGGATGAGATGATCATGAGCTTTAAATGTCGGGATTTATCGA 465
 Db 1380 GAGGCAATTAACATTTGATGGGAGGATATTAGGAACCTTTAATGTAAACTATCTGAGG 1439
 Qy 466 GACCATATGGAGTGGTTAGTCAAGAGCTGTTTGTTCGGGAGCCACCATCAGTAACAT 525
 Db 1440 GAATCATGTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1499
 Qy 526 ATCAAGTATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 585
 Db 1500 ATTTGTTATGCGGTGGAATGTAACCATGATGATGATGATGATGATGATGATGATGATGATG 1559
 Qy 586 AATGCTGATGATTTTATCATGAGTTCCTTAATTAATTTATATATATATATATATATATATAT 645
 Db 1560 AACGCTATGATGTTTATCATGAAATTTACCAAGAAATTTGACACCTGTTGGAGAGAGA 1619
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 Qy 706 AACCCCAAGATTTGATTTTATGATGAGCTAGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTG 765

Db 1680 AACCCCAAGATCTCTTCTGCTGGATGAGGCCACGTGACGATTTGGACACAGAAAGTGAAGCT 1739
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Db 1740 GAGGTACAGGAGCTCTGATATAGCCAGAGAGCGCGGACCACCATTTGATAGCACAC 1799
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Db 1800 CGACTGTCTACGGTCCGAAATGCGAATGTCATGCTGGTGTGAGGATGGAATTTGTG 1859
Qy 886 GAGAAAGAGGACATGCTGAATTAATGCAAAAGAGCTCTATATTACTTCTGTCAT- 944
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Qy 945 -----GTCCAGAGATATTAAAAAGCTGATGAAACAGATG 978
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Qy 1573 TTTATATATGATGGGAGATGACATTCCTGATCTGATATTGCTCCAGTACTTGGCGTG 1632
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Db 2940 TTCAGAGATGTTATTTCTGGTGTCTGCAATTTGATTTGGTGCAGTGGCTTAGGACAT 2999
Qy 1993 AGCTCGTTTGGCTTCTGAAATATTCCAAAGCCAAATCGGGGCTCGGCACTGTTTGGCC 2052
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Qy 2113 TGTGAAGGAATTTAGAGTTTCGAGAAAGTCTCTTTCTTCTATCCATGTCGCCAGATGTT 2172
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Qy 2233 AGCAGCGGCTTGGGAAAGCACTTCTGTTCAACTTCTGACAGACTTTTATGACCCCGTG 2292
Db 3240 AGCAGTGGCTTGGGAAAGACAGCGGTGCTCAGCTCTCTGGAGCGGTTCTACGACCCCTG 3299
Qy 2293 CAAGGACAGTCTGTTGATGTTGGATGCAAAAGAAATTCAGTGTACAGTGGCTCCGT 2352
Db 3300 GCGGGGACAGTGTCTTCGATGTTCAAGAGCAAAAGAACTCAATGTCAGTGGCTCAGA 3359
Qy 2353 TCCAAAATAGCAATCGTTCTCCTCAAGAGCCTGTGCTCTTCAACTGACAGCACTTCTGAGAAC 2412
Db 3360 GCTCAACTCGGAATCGTGTCTCAGGAGCTATCTTATTGACTGACAGCACTTCCGAGAAT 3419
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Db 3420 ATTGCTTATGAGAGACACAGCGGCTGTGATCACAGGATGAAATTTGAGTGCAGCCAAA 3479
Qy 2473 GCAGCAATATCCATTTCTTTTATGAAAGCTCTCCTGAGAAATACAAACAAAGTTGGA 2532
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Qy 2593 CTCCAAAACCCAAAATTTTATTGTTGGATGAGGCACTTCAGCCCTCGATATGACAGT 2652
Db 3600 ATCAGACACCTCAATCTCTCTGTTGGATGAGCTACATCAGCTCTGATCTGAAAGT 3659
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Db 3780 GTCAAGGAGCTGCGACATGCAAGCTGCTGCGACAGAAAGGCTATCTTTTCAATG 3839
Qy 2833 GTGAATGCACTCAGTG 2850
Db 3840 GTCAGTGTCCAGGCTGGG 3857

RESULT 12

US-09-306-417-1
 ; Sequence 1, Application US/09306417
 ; Patent No. 6548301
 ; GENERAL INFORMATION:
 ; APPLICANT: Heinrich-Pette-Institut
 ; TITLE OF INVENTION: Retroviral Gene Transfer Vectors
 ; FILE REFERENCE: P50491
 ; CURRENT APPLICATION NUMBER: US/09/306,417
 ; CURRENT FILING DATE: 1999-05-06
 ; EARLIER APPLICATION NUMBER: DE 198 22 115
 ; EARLIER FILING DATE: 1998-05-08
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 8630
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: proviral
 ; OTHER INFORMATION: plasmid DNA
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)..(160)
 ; OTHER INFORMATION: plasmid backbone (pUC)
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (161)..(677)
 ; OTHER INFORMATION: 5'-LTR
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (512)..(1219)
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: (1220)..(5062)
 ; OTHER INFORMATION: m4 mdr-1 cDNA
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (5215)..(5774)
 ; OTHER INFORMATION: 3'-LTR
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (5775)..(8630)
 ; OTHER INFORMATION: plasmid backbone (pUC)
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)..(8630)
 ; OTHER INFORMATION: retroviral expression vector SFbeta71m4

Query Match 36.0%; Score 1027; DB 4; Length 8630;
 Best Local Similarity 62.1%; Pred. No. 3e-287;
 Matches 1693; Conservative 0; Mismatches 990; Indels 42; Gaps 3;
 QY 166 ATATTGTAAGAAACCCAGTATAGTAACCTTTCCACAGCTGGATATAAACCCTGAATCC 225
 DB 2321 ATATTGTAAGAAACCCAGTATAGTAACCTTTCCACAGCTGGATATAAACCCTGAAT 2380
 QY 226 ATAGAGGAACTCTGGAAATTTAAATGTTTCTTCAATATCCATCAAGACCACTATC 285
 DB 2381 ATTAGGGAAATTTGGAAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAGAGTT 2440
 QY 286 AGATTCTGAAGGCTTGAATCTCAGAAATTAAGTCTGGAGAGACAGTGCCTTGGTCGGT 345
 DB 2441 AAGATCTTGAAGGCTTGAATCTCAGAAATTAAGTCTGGAGAGACAGTGCCTTGGTCGGT 2500
 QY 346 CTCATGGCAGTGGGAGAGTACGGTAGTCCAGCTTCTGACAGGTTATATGATCCGGAT 405
 DB 2501 AACAGTGGCTGGGAGAGTACGGTAGTCCAGCTTCTGACAGGTTATATGATCCGGAT 2560
 QY 406 GATGCTTTATCATGCTGAGATGAGATGATCATCAGAGCTTTAAATGTGGCGCATATCGA 465

2561 GAGGGGATGTCAGTGTGATGGACAGGATATTAGGACCATATAAATGTAAGGTTTCTACGG 2620
 466 GACCATATTGGAGTGGTTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAAAT 525
 2621 GAAATCAITGGTGTGGTGCAGGAACTGTTATGTTTGGCCACCAACCATAGTCAAAAC 2680
 526 ATCAAGTATGACAGAGATGATGTAAGTATGAGAGATGAGAGAGAGAGAGAGAGAGAG 585
 2681 ATTGCTATGCGCGTGAATAATGTCAACATGATGAGATGAGAGAGAGAGAGAGAGAGAG 2740
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 2861 AACCCCAAGATTTAGATGAGGCTACGCTGCGCTGGATTGAGAAAGCAAGTCA 2920
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 886 GAGAAAG 945
 3041 GAGAAAG 3100
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 998 -----CTGAAAG 1045
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 1046 -----AGTCAAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
 3221 ACTGATAGGAGTGTCCGTGGATCAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3280
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 3341 TGGCTTTTGGTCTGGGAG 3400
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 3521 ATTAACATTTTCTTCAAGGTTTTCACATTTGGCAAGAGAGAGAGAGAGAGAGAGAG 3580
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 3581 CTCGATACATGGTTTTCGATCCATGCTCAGACAGAGAGAGAGAGAGAGAGAGAGAG 3640
 1444 GAAACAGCAG 1503
 3641 AAAAACCAACCTGAGAGATTTGACTTACCAGGCTCGCCCAATGATGCTGCTCAAGTTAA 3700

Qy	226	ATAGAAGAACTGTGGAAATTTAAAAATGTTCTTTTCAATATATCATCAAGACCAATCTATC	285
Db	1586	ATTAAAGGGAATTTTGGAAATTCAGAAATGTTCACTTTCAGTTTACCCATCTCGAAAAGAAAGTT	1645
Qy	286	AAGATTCTGAAAGGCTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTCGCTTCGTGCGGT	345
Db	1646	AAGATCTTGAAGGCCCTGAACTTGAAGTGCAGATGGCGACAGCGTCCCCCTGGTTGGA	1705
Qy	346	CTCAATGGCAGTGGGAAGAGTACGGTATGTCAGCTTCTGCAGAGGTTATATGATTCGGAT	405
Db	1706	AACAGTGGCTGTGGGAAGAGACAAACAGTCCAGCTGATGCAGAGGCTCTATGACCCACCA	1765
Qy	406	GATGGCTTTATCATGGTGGATGAGAAATGACATCAGAGCTTTAAATGTGCGCATTTATCGA	465
Db	1766	GAGGGATGGTCAGTGTTTCATGGACAGGATATAGGACCAATAATGTAAAGTTTCTACGG	1825
Qy	466	GACCAATATGGAGTGGTTAGTCAAGAGCCGTGTTTGTTCGGACCAACCATCAGTAAACAAT	525
Db	1826	GAATATCATTTGGTGTGGTGAAGTCAAGAACCTGTATTTGTTGCCACCAAGATAGCTGAAAC	1885
Qy	526	ATCAAGTATGACGAGATGATGTCACTGATGACAGATGCGAGAGCAGCAGCAAGCGGAGCA	585
Db	1886	ATTGCTATGGCCGTGAAATGTCCACATGATGAGATTCAGAAAGCTGTCAAGGAAGCC	1945
Qy	586	AATCGCTGATTTTATCATGGAGTTTCTTAATAAATTTAATCATTTGGTAGGGGAAAAA	645
Db	1946	AATGCCATTGACTTTATCATGAAACTGCCTCATAAATTTGCACCCCTGGTTGGAGAGAGA	2005
Qy	646	GGAGCTCAATAGTGGAGGGCAGAAACAGAGATCCCAATTCCTGTCGCTTAGTTTGA	705
Db	2006	GGGCCCCAGTTAGTGTGGGCGAAGCAGAGGATCCCAATTCACGTGCGCCCTGGTTGCG	2065
Qy	706	AACCCCCAAGATTTCTGATTTTTAGATGAGGCTACGTTCTGCCCTGGATTCAAGAAACGACATCA	765
Db	2066	AACCCCHAGATCCTCTCTGCTGGATGAGGCCACGTCAGCTTGGACACAGAAAGCGAGCA	2125
Qy	766	GCTGTTCAAGCTGACATGAGAGAGCGCAGCAAAAGGTCGACACTACATCGTGTGAGCACAC	825
Db	2126	GTGCTTCAGGTGGCTCTGAGTAAGGCCAGAAAAGGTCGACCCACCATTTGTGATAGCTCAT	2185
Qy	826	CGACTTCTACTATTTCGAATGTCAGATTTTCGATTTGTGACCCCTAAAGGATGGAATCTGGCG	885
Db	2186	CGTTTGTCTACGTTTCTGAATGCTGACGTCATCTGCTGTTTCGATGATGAGTCAATTGTG	2245
Qy	886	GAGAAAGGACACATCTGAACTAATGGCAAAACGAGGCTCTATATTATTCATTTGTGATG	945
Db	2246	GAGAAAGGAAATCATGATGAACTCATGAAAGAGAAAGGCAATTTACTTCAAACCTGTCA	2305
Qy	946	TCACAGGATATTAAAAAGCTGATGA-----CAGATGGAGTCAATGACATA	992
Db	2306	ATGCAGACACGAGGAATGAAGTTGAATTAGAAAAATGCACGCTGATGAATCCAAAAGTGAA	2365
Qy	993	TTCTACTGAAGAAAGAACCAACTCACTTCCTCTGCACTCTGTGAAGAGCATCAAGTCAGA	1052
Db	2366	ATTGATGCTTGGAAATGCTTCAAATGATTCAAGTACAGTCTTAATAAGAAAGATCA	2425
Qy	1053	CTTCATTGACAGGCTGAGGAATCCACC-----AATCT	1086
Db	2426	ACTCGTAGGAGTGTCCGTGGATCACACCCCAAGAGAGCTTAGTACCAAAGAGGCT	2485
Qy	1087	AAAGAGATAAGTCTTCTCTGAAGTCTCTCTATTTAAATAATTTTAAAGTTAAACAAGCCTGAA	1146
Db	2486	CTGGAATGAAGTATACCTCCAGTTTCTTTTGGAGGATATGAGCTTAATTTAACTGAA	2545
Qy	1147	TGGCCTTTTGTGTTCTGGGAATTTGGCTCTCTGTTCTTAAATCGAACTGTTCAATCAGTA	1206
Db	2546	TGGCCTTATTTGTTGTGTGTATTTTGTGCCATTATTAATGGAGCCCTGCAACAGCA	2605
Qy	1207	TTTTTCCATCATCTTTGCAAAAATATTAACCATGTTTGGAAATATGATAAAACCATTA	1266
Db	2606	TTTGCATAATATATTTCCAAAGATATAGGGGTTTTTACAGAAATTGATGATCTCGAACA	2665
Qy	1267	AAG---CATGATCGAGAAATTTAFTCAATGATATTCGTCAATTTTGGGTGTTATTTGCTTT	1323

[illegible]

Db 3746 TGGCTCCGAGCACACCTGGGCGATCGTGCCAGGAGCCCATCTCTGTTGACTGCAGCAT 3805
Qy 2404 GCTGAGAACATCGCTTATGGTGAACAAGCGCGTGTGTGCCATTAGATGAGATCAAGAA 2463
Db 3806 GCTGAGAACATCGCTTATGGTGAACAAGCGCGTGTGTGCCATTAGATGAGATCAAGAA 3865
Qy 2464 GCCCAATGAGCAATATCCATTCTTTTATGAAGTCTCCCTGAGAAATACACACA 2523
Db 3866 GCAGCAAGGAGGCAACATACATGCGCTTCATCGAGTCACTGCTATATATATAGCACT 3925
Qy 2524 CAGTTGAGCAAGGAGGAGCAAGCTTCTTGCGCGGCGAGAAAACAAAGACTAGCTATTGCA 2583
Db 3926 AAGTAGGAGCAAGGAGGAGCAAGCTTCTTGCGCGGCGAGAAAACAAAGACTAGCTATTGCA 3985
Qy 2584 AGGCTCTCTCCCAAAACCCAAATTTATTTGATGAGGCGCACTTCAGCGCTCGAT 2643
Db 3986 CGTCCCTCTGTAGACAGCCTCATATTTGCTTTGATGAGGCGCACTTCAGCTCTGAT 4045
Qy 2644 AATGACAGTGAAGAGTGGTTTTCAGATGCGCTTCAATGAAGCGAGGAGCGGAGCAATGC 2703
Db 4046 ACAGAAAGTGAAGAGTGGTTTTCAGATGCGCTTCAATGAAGCGAGGAGCGGAGCAATGC 4105
Qy 2704 CTAGTGGTCACTCAGGCTCTCTGCAATTCAGAACGCGATTTGATGCTTCTGCAC 2763
Db 4106 ATTGATGCTCAGCGCTCTCCACATCCAGATGCGACTTATATAGTGGTTCAG 4165
Qy 2764 AATGGAAGATTAAGGAGCAAGGAACTCATCAAGAGCTCTGAGAAATCGAGACATATAT 2823
Db 4166 AATGCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4225
Qy 2824 TTTAAGTATGATGACAGTCTAG 2848
Db 4226 TTTTCAATGGTCACTGCTCCAGCCTG 4250

RESULT 14

US-08-752-447-1
; Sequence 1, Application US/08752447
; Patent No. 5994888
; GENERAL INFORMATION:
; APPLICANT: Mechnether, Eugene
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehner Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,447
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5994088nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-9808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..424
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 425..4264
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 4265..4669
; US-08-752-447-1

Query Match 35.8%; Score 1022.2; DB 2; Length 4669;
Best Local Similarity 62.0%; Pred. No. 5.2e-286;
Matches 1690; Conservative 0; Mismatches 993; Indels 42; Gaps 3;

Qy 166 ATTATTGATGAAGAACCCAGTATAGATAACTTTTCCACAGCTGGATATATAAACCCTGATCC 225
Db 1526 ATAATTGATGAAGAACCAAGTATTGACAGTATTGGAAGAGTGGGCACAAACAGATAAT 1585
Qy 226 ATAGAAGGAACGTGTGAATTTTAAATGTTCTTTCAATTATCCATCAAGACCATCTATC 285
Db 1586 ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTACCATCTCGAAGAAGT 1645
Qy 286 AAGATTCTGAAGGCTCTGAATCTCAGAAATTAAGTCTGGAGAGACAGTGCCTTGGTCCGT 345
Db 1646 AAGATCTTGAAGGCTCTGAACCTGAGGTGACAGAGTGGGCAGACGCTGCTGCTGTTGA 1705
Qy 346 CTCATATGGCAGTGGGAGAGTACGGTAGTCCAGCTTCTCAGAGGTTATATATCCGGAT 405
Db 1706 AACAGTGGCTTGGGAGAGGACACAGTCCAGCTGCTGAGAGGCTCTATGACCCACA 1765
Qy 406 GATGGCTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTGGCGCATTTATCA 465
Db 1766 GAGGGATGCTCAGTCTTGTATGAGCAGGATATTAGGCCATAAATGTAAGTTTCTACGG 1825
Qy 466 GACCATATTGGAGTGGTGTAGTCAAGAGCCTGTTTCTCGGGACCAACCATCAGTACCAAT 525
Db 1826 GAATCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1885
Qy 526 ATCAAGTATGAGCAGATGATGTGACTGATGAAGAGATGAGAGATGAGAGAGGAGGAGCA 585
Db 1886 ATTGCTATGGCGCTGAAAATGTCCACATGATGAGATTGAGAAAGCTGTCAAGGAAGCC 1945
Qy 586 AATGCTATGATTTTATCATGAGGTTTCTTAATAAATTTAATACATTTGTTAGGGGAAAA 645
Db 1946 AATGCTATGATTTTATCATGAGGTTTCTTAATAAATTTGACACCTGTTGGAGAGAG 2005
Qy 646 GAGAGCTCAATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 705
Db 2006 GGGGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2065
Qy 706 AACCCCAAGATTTCTGATTTTATGATGAGGCTAGTCTGCGCTGGATTCAGAAAGCAAGTCA 765
Db 2066 AACCCCAAGATTTCTGATTTTATGATGAGGCTAGTCTGCGCTGGATTCAGAAAGCAAG 2125
Qy 766 GCTGTTCAAGCTGCACTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825
Db 2126 GTGTTTCAAGTGGCTCTGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2185
Qy 826 CGACTTTTCTACTATTCGAAGTGCAGATTTGATTTGAGCCCTTAAAGGATGGAATGCTGGCG 885
Db 2186 CGTTTGTCTACAGTTTCTGATTAAGTGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245
Qy 886 GAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
Db 2246 GAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2305
Qy 946 TCACAGGATATTAAAAAGCTGATGAACAGAGTGAAGTCAATGACATATTCTA----- 997
Db 2306 ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAAATGACAGTGTGATGAATCCAAAAGTGA 2365

QY 998 -----CTGAAGAAAGACCAACTCCTCTCTGCACTCTGTGAAGACATCA--- 1045
Db 2366 ATTGATGCCCTTGGAAATGCTTCAATGATTCAGATCCAGTCTAATAGAAAAGATCA 2425
QY 1046 -----AGTCAGACTCAITGACAGGCTGAGAAATCCACCCAAATCT 1086
Db 2426 ACTCGTAGAGTGTCCGTGGATCACAAGGCCCAACACAGAAAGCTTAGTACCAAGAGGCT 2485
QY 1087 AAAGACATAGCTCTCTGAAGTCTCTCTAATAAATAATTTAAAGTAAACCAAGCTGAA 1146
Db 2486 CTGGATGAAGATATCTCAGTTTCTTTTGGAGATTTATGAGCTAAATTAATCTGAA 2545
QY 1147 TGGCCCTTTTGTGGTCTTGGGACCAITGGCTTCTGTTCTAAATGGAACTGTTTCAATCCAGTA 1206
Db 2546 TGGCCCTTAATTTGTGGTGTATTTGGGCCAATTAATAATGAGGCCCTGCAACCCAGCA 2605
QY 1207 TTTTCCATCATCTTCCAAATAATATAACCATGTTTGGAAATAATGATAAACCACATTA 1266
Db 2606 TTTGCAATAATATTTTCAAGATATAGGGGTTTACAGAAATGATGATCTGAAACA 2665
QY 1267 AAG---CATGATCAGAAATTTATTCATGATATTCCTCATTTTGGGTGTATTTGCTTT 1323
Db 2666 AAACGACAGATAGTAATCTTTTACATTTCTAGCCCTTGGAAATTAATTTCTTTT 2725
QY 1324 GTGAGTTATTTATGAGGATATTTTACGAGAGAGGGAATTTTACGATGAGA 1383
Db 2726 AHTACATTTTCTTTCAGGGTTTTCATTTGGCAAGCTGGAGAGATCTCCACCAAGCG 2785
QY 1384 TTAAGACACTTGGCCCTTCAAGCCATGTTATATCAGGATATTCCTGTTTGTATGAAAG 1443
Db 2786 CTCGATACATGTTTCCGATCCATGCTCAGACAGAGATGAGTTGTTTCAAGCCCT 2845
QY 1444 GAAAACGACAGAGGCTTGAACAATAATTTAGCCATGATATAGCAATAATTTAAGGA 1503
Db 2846 AAAAAACCACTGAGCATTTACTACAGCTGCGCAATGATGCTCTCAAGTTAAAGG 2905
QY 1504 GCAACAGGTTCCAGGATGCGCTTCTAAACAAAATGCAAACTAACTGGGACTTTTCAGTT 1563
Db 2906 GCTATAGGTTCCAGGCTTCTGTAATTAACCAATATAGCAATCTTGGACAGGAATA 2965
QY 1564 ATCATTTCTTTATATAGAGGAGATGACATTCCTGATTCAGATTTGCTCCAGTA 1623
Db 2966 ATTATATCTTCTATCTATGTTGGCACTTAACACTGTTACTCTTGAATTTGACCCATC 3025
QY 1624 CTTGCGGTGACAGGATATGAAACCGGCAATGACTGGATTTGCCAACAAGATAG 1683
Db 3026 ATTGCAATAGCAGGATGTTGTAATGAAATGTTTGGTGGCAAGCACTGAAAGATAAG 3085
QY 1684 CAAGAACTTAAGCATCTGGAAGATAGCAACTGAAGCTTTGGAGATATAGCTACTATA 1743
Db 3086 AAAGAACTAGAGGCTGCTGGAGATCGCTACTGAAGCAATAGAAACTTCCGAACCGTT 3145
QY 1744 GTGTCAATTAACAGGAAAGCCCTTCGAGCAATGTTATGAGAGATGCTTCAGACTCAA 1803
Db 3146 GTTCTTTGACTCAGAGCAGAAAGTTTGAACATATGATGTTGCTCAGAGTTTGCAGGTA 3205
QY 1804 CACAGAAATACCTCGAAGAAAGCACAGATTTATGGAAGCTGTTATGCAATTCAGCCATG 1863
Db 3206 TACAGAACTCTTTGAGAAAGCACACATCTTGGAAATTAATTTCTTCCACCGAGCA 3265
QY 1864 TTTATATATTTTGGCTATGACAGGCTTTCGATTTGGAGCCCTATTTAAATCAAGCTGA 1923
Db 3266 ATGATGTAATTTTCCCTATGCTGATGTTTCCGGTTTGGAGCCCTACTTGGTGGCACATAAA 3325
QY 1924 CGAATACCCACAGAGGCTGTTTCAATGTTTACTGCAATTCATGATGAGTATGGCC 1983
Db 3326 CTATGAGCTTTGAGGATGTTCTGTAGTATTTTTCAGCTGTTGCTTGTGCTCATGGCC 3385
QY 1984 ATCGGAAACAGCTCGTTTGGCTCTCTGATATTTCCAAAGCCAAATTCGGGGCTGGCAT 2043
Db 3386 GTGGGCAAGTCACTTTCATTTGCTCTCTGACTATGCAAGCCAAATATATCAGCAGCCAC 3445
QY 2044 CTGTTTGGCTTGTGGAAGAAACCAATATAGACAGCGCGAGTCAAGAGGGAAG 2103

Db 3446 ATCATCATGATCATTTGAAAAAACCCCTTTGATTGACAGCTACAGCGAAGGCCTATG 3505
QY 2104 CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTTCTTCATCTGTC 2163
Db 3506 CCGAACACATTTGGAGGAATTTGTCATTTGGTGAAGTTGTTATCAACTATATCCCAACCG 3565
QY 2164 CCAGATGTTTTCATCTCCGTGGCTTTATCCCTCAGTATTGAGCGAGGAAGACAGTAGCA 2223
Db 3566 COGACATCCCACTGCTTCAGGACTGAGCTCGGAGTGAAGAGGCCAGACGCTGGCT 3625
QY 2224 TTTTGGGAGCAGCGGCTGTGGGAAAAGCACTTCTGTTCACCTTCTCTCAGAGACTTTAT 2283
Db 3626 CTGGTGGCAGCAGTGGCTGTGGGAAAGCAAGTGGTCCAGCTCTCTGGAGCGGTTCTAC 3685
QY 2284 GACCCCTGTCAAGGCAAGTGTCTGTGATGTGTGGAATCAAAAGAAATGAATGACAG 2343
Db 3686 GACCCCTTGGCAGGAAGTGTCTGTGATGGAAGAAATTAAGCGACTGATGTTTCAG 3745
QY 2344 TGGCTCCCTTCCCAATATAGCAATCGTTCTTCAAGAGCCTGTCTTCAACTGCGACAT 2403
Db 3746 TGGCTCCGAGCACACTGGGCACTGTGTCCAGGAGCCCTCTCTTGTGACTGCGACAT 3805
QY 2404 GCTGGAACATCGCTATGTGTGCAACAGCGTGTGTGCGCATTTAGTGTGATCAAGAA 2463
Db 3806 GCTGGAACATTTGCTATGAGAGCAACAGCGGTGTGTGACAGAAAGATCTGTGAG 3865
QY 2464 GCGCAAAATGCAAGCAATATTCATTTTATGGAAGTCTCCCTGAGAAAATACACACA 2523
Db 3866 GCAGCAAGGAGGCCAACAATACATGCTTCATCGAGTCACTGCTTAATAAATATAGCA 3925
QY 2524 CAGTTTGAATGAAAGGAGCAGCTTCTGCGCGCCAGAAAACAAGACTAGCTATTGCA 2583
Db 3926 AAAGTAGGAGCAAGAGAACTCAGCTCTCTGGTGGCCAGAAAACAACGCAATGCGCAT 3985
QY 2584 AGGGCTCTTCTCCAAAAACCCAAATTTATTTGATGAGGCGCACCTTCAGCCCTCGAT 2643
Db 3986 GTCGCTTTTGTAGACGCTCATATTTGCTTTTGGATGAAGCCACGCTCAGCTGGAT 4045
QY 2644 AATGACGTGAGAGTGGTTTCAAGATCCCTTGTATTAAGCCAGGACGGGAAGCATG 2703
Db 4046 ACAGAAAGTGAAGAGTTTGTCCAAAGAGCCCTGCAAGCCAGAGAAAGCCGCGCACCT 4105
QY 2704 CTAGTGGTCACTCAGAGCTCTCTGCAATTCAGAACGCAAGATTTGATAGTGTCTG 2763
Db 4106 ATTGATTTGCTCAGCGCTGTCCACCATCCAGATGCGAGCTTAATAGTGTGTTTCA 4165
QY 2764 AATGAAAGATAAAGGAACAAGAACTCATCAAGAGCTCTTGAGAAATCGAGACATAT 2823
Db 4166 AATGCAAGTCAAGAGCATGGCAAGCATCAGAGCTGCTGCGACAGAAAGGCAATCAT 4225
QY 2824 TTTAAGTTAGTGAATGCACTCAG 2848
Db 4226 TTTCAATGGTCAAGTGTCCAGGCTG 4250

RESULT 15

US-09-316-167-1

; Sequence 1, Application US/09316167

; Patent No. 6365357

; GENERAL INFORMATION:

; APPLICANT: Mechetner, Eugene

; APPLICANT: Roninson, Igor B

; TITLE OF INVENTION: Methods and Reagents for Preparing and

; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESS: McDonnell Boenken Hulbert & Berghoff Ltd.

; STREET: 300 South Wacker Drive, Seventh Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,167
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 636537nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-09-316-167-1

Query Match 35.8%; Score 1022.2; DB 4; Length 4669;
Best Local Similarity 62.0%; Pred. No. 5.2e-286;
Matches 1690; Conservative 0; Mismatches 993; Indels 42; Gaps 3;

QY 166 ATATTGATAGAAACCCAGTATAGATAAATTTTCCACAGCTGGATATAACCTGAATCC 225
Db 1526 ATATTGATATAAGCCAAAGTATTGACAGCTATTGGAAGTGGCGCAAAACAGATAAT 1595

QY 226 ATAGAGGAAGCTGGGAATTTAAATATGTTTCTTCAATTCATTCATCCAGACCATCTATC 285
Db 1586 ATTAAGGGAAATTTGGAAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAGAGTT 1645

QY 286 AAGATTCTGAAGGCTCGAATCTCAGAATTAAGTCTGGAGAGACAGCTCCCTTGGTGGT 345
Db 1646 AAGATCTTGAAGGCTCGAATCTCAGAATTAAGTCTGGAGAGACAGCTCCCTTGGTGGT 1705

QY 346 CTCAATGGCAGTGGGAAGTACGGTAGTCCAGCTTCTGCGAGAGTATATATGATCCGGAT 405
Db 1706 AACAGTGGCTGGGAAGAGCAACACAGTCCAGCTGATGCGAGAGCTCTATGACCCACA 1765

QY 406 GATGCTTTATCATGCTGGATGAGATGACATCAGAGCTTTAAATGTGCGGCATTATCGA 465
Db 1766 GAGGGATGCTGCTGTTGATGGACAGATATAGACCAATATGTAAGTCTTACGG 1825

QY 466 GACCATATTGGAGTGGTATTAGTCAAGAGCTGTTTGTTCGGAGCAACATCAGTAACAAT 525
Db 1826 GAAATCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1885

QY 526 ATCAAGTATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
Db 1886 ATTCGCTATGGCCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1945

QY 586 AATGGCTATGATTTTATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 645
Db 1946 AATGGCTATGATTTTATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2005

646 GGAGCTCAAAATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 705
2006 GGGGCCAGTGTGAGTGGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2065

706 AACCCCAAGATTCTGATTTTGAATGAGGCTACGTTGCGCTGGAATTCAGAAAGCAAGTCA 765
2066 AACCCCAAGATCTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2125

766 GCTGTTCAAGCTGACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
2126 GTGGTTCAAGTGGCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2185

826 CGACTTTCTACTATTCGAAGTGCAGATTTGATGACCTTAAGGAGTGAATGCTGGCG 885
2186 CGTTTGTCTACAGTTCGTAATGCTGACGTCATCGCTGGTTCGATGATGAGTCAATGTG 2245

886 GAGAAAGGAGCAGATCTGAACTTAATGGCAAAAGAGGCTCTATTTATTTTCACTTTGATG 945
2246 GAGAAAGGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2305

946 TCACAGGATATTAAAAAGCTGATGAACAGATGAGGATCAATGACATATTTCTA 997
2306 ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAATGACAGCTGATGAATCCAAAGGAA 2365

998 -----CTGAAAGAGAGCCAACTCACTCTCTGCACTCTGTCAGAGAGATCA--- 1045
2366 ATTGATGCTTGGAAATGCTTCAAAATGATTCAGATCCAGTCTAATAGAAAAGATCA 2425

1046 -----AGTCAGACTTCAATTCAGCAAGGCTGAGGAATCCACCCATCT 1086
2426 ACTGCTAGGAGTGTCTGATGATCAAGGCCAACACAGAAAGCTTAGTACCAAGAGGCT 2485

1087 AAGAGATAGTCTTCTGAGTCTCTCTATTTAAATTTTAAAGTTAAACAGCTGAA 1146
2486 CTGGATGAAAGTATACCTCCAGTTCTTTTGGAGGATTTATGAAGCTAAATTTAACTGAA 2545

1147 TGCCCTTTTGTGGTCTGGGCAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1206
2546 TGCCCTTTTGTGGTCTGGGCAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2605

1207 TTTTCCATCATCTTTGCAAAATTAATACCATGTTTGGAAATTAATGATTAACCAATTA 1266
2606 TTTGCAATTAATTTTCAAAAGTATTTAGGGGTTTTCAGAAATTTGATGATCTCGAAACA 2665

1267 AAG---CATGATGACAGAAATTTATTCATCATGATTTCTTCTTCTTCTTCTTCTTCTTCT 1323
2666 AAAGCAGAAATGATTAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2725

1324 GTCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1383
2726 ATTACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2785

1384 TTAAGACACTTGGCTTCAAGCCATGTTATATCAGATATTGCTGTTTCTTCTTCTTCTTCTTCT 1443
2786 CTCGATACATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2845

1444 GAAAAACAGCAGAGGCTTTGACAAATTAATTAAGCCATAGATATAGCAAAATTCAGGA 1503
2846 AAAAAACACACTGAGCATTTGACTACAGGCTCGCAATGATGCTGCTCAAGTTAAAGGG 2905

1504 GCAACAGTTCAGGATTTGGCTTTTAAACAAATGCAAAATGCAAAATGCAAAATGCAAAATGCA 1563
2906 GCTATAGTTTCCAGGCTTGTCTGTAATTTACCCAGATATAGCAAAATTTGGACAGGATA 2965

1564 ATCATTTCTTTATATATGATGAGGAGATGACATTTCTGATTTCTGATGATTTCTGATGAT 1623
2966 ATTATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3025

1624 CTTGCGCTGACAGGATGATTTGAAACCGGCGCAATGATGATGATTTGCCCAAGATAG 1683
3026 ATTGCAATAGCAGGATTTGTTGAATTTGAATTTGTTGCTGGACAGACACTGAAAGATAAG 3085

1684 CAAGAACTTAAGCATCTGCGAAAGATAGCAACTGAAAGCTTTGGAATATATACGTACTATA 1743

Db 4166 AATGGCAGAGTCAAGGAGCATGGCAGCATCAGCAGCTGTGGCACAGAAAGGCATCTAT 4225
Qy 2824 TTTRAAGTTAGTGAATGACAGTCTAG 2848
Db 4226 TTTTCAATGGTCAAGTGTCCAGGCTG 4250

Search completed: June 25, 2004, 03:53:26
Job time : 241 secs

Db 3086 AAAGAACTAGAGGTGCTGGAGATCGCTACTGAAGCAATAGAAACTTCGGAACGGTT 3145
Qy 1744 GGTCTATTAAACAGGGAAGCCCTTCAGCAATGTATGAAGAGATGCTTCAGACTCAA 1803
Db 3146 GTTCTCTTGACTCAGGAGCAGAGTGAACATATATATGCTCAGAGTTTGAGGTACCA 3205
Qy 1804 CACAGAAATACCTCGAAGAAACACAGATTATGGAAGCTGTATGCAATTCAGCCATGCC 1863
Db 3206 TACAGAACTCTTTGAGGAAGCACACATCTTTGGAATTACATTTCTTCAACCCAGGCA 3265
Qy 1864 TTTATATATTTGCCATGACAGAGGTTTCGATTTGAGGCTTATTTAATTAAGCTGGA 1923
Db 3266 ATGATGATATTTTCTATGCTGGATGTTCCGGTTTGGAGCTTACTTGGTGGCACATAA 3325
Qy 1924 CGAATGACCCACAGAGGCAATTCATAGTTTCTTACTGCAATTCATATGAGCTATGGCC 1983
Db 3326 CTATGAGCTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTGTTGTTGTCATGGCC 3385
Qy 1984 ATCGGAAAAACGCTCGTTTGGCTCCTGGAATATTCGAAAGCCAAATTCGGGGGCTGCGCAT 2043
Db 3386 GTGGGCAAGTCAGTTTCTTGTCTGCTGACTATGCAAGGCCAAATATCAGCAGGCCAC 3445
Qy 2044 CTGTTTGCCTTGTGGAAGAACCAATATAGACGCGCAGTCAAGAGGGGAAG 2103
Db 3446 ATCATCATGATCATTTGAAAAACCCCTTTGATTTGACAGCTACAGCAGGAGGCCCTATG 3505
Qy 2104 CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAGTCTCTTTCTTCTATCCATGTGC 2163
Db 3506 CCGAACACATTTGAGGAATGTACATTTTGTGAGTTGTATTCACATATCCACCCGA 3565
Qy 2164 CCAGATGTTTTCATCTCCGTGGCTTATCCCTGATATTGAGCGGGAAGACAGTAGCA 2223
Db 3566 CCGACATCCAGTGCTTCAGGGACTGAGCTGGAGTGAAGGGGCCAGAGCTGGCT 3625
Qy 2224 TTTGTGGGAGCAGCGGCTGTGGGAAAGCACTTCTTCAACTTTCGACAGACTTTAT 2283
Db 3626 CTGGTGGGACAGTGGCTGTGGAGAGCACAGTGTCCAGCTCCTGGAGCGGTTCTAC 3685
Qy 2284 GACCCCTGCAAGACAGAGTGTCTTTGATGGTGTGATGCCAAAGAAATTAATGTACAG 2343
Db 3686 GACCCCTTGGCAGGGAAGTGTCTTTGATGGCAAGAAATAAAGCGACTGAATGTTCAG 3745
Qy 2344 TGGCTCGTTCCCAATAGCAATCGTTCTCAAGAGCTGTGCTTCTCAACTGCGCAT 2403
Db 3746 TGGCTCCGAGCACACCTGGGCAATCGTGTCCAGAGGCCATCTGTTTGAATGAGCAT 3805
Qy 2404 GCTGAGAACATTCGCTATGTGACACAGCGGTTGTGGCCATTAGATGAGATCAAGAA 2463
Db 3806 GCTGAGAACATTCGCTATGAGACACAGCGGTTGTGTCAAGGAAGAGATCGTGAGG 3865
Qy 2464 GCCGCAATGACAGCAATTCCTTTTATTGAAGTCTCCCTGAGAAATACACACA 2523
Db 3866 GCAGAAAGGAGGCCAACATACATGCTTCAATCGAGTCACTGCTTAATAATATAGCAT 3925
Qy 2524 CAAGTTGACTGAAAGGAGCACAGCTTTCTGGCGGCCAGAAACAAAGACTAGCTATTGCA 2583
Db 3926 AAAGTAGGAGACAAAGGAACTCAGCTCTCTGGTGGCCAGAAACAAAGCATTTGCCATAGCT 3985
Qy 2584 AGGGCTCTTCTCAAAAACCCAAATTTTATTTGATGAGGCCACTTCAGCCCTCGAT 2643
Db 3986 CGTGGCTTGTAGACAGCTCATATTTGCTTTTGGATGAAGCCACGTCACTCTGGAT 4045
Qy 2644 AATGACAGTGAAGGTGTTTCAGATGCCCTTGTATTAAGCCAGGACGGGAAGGACATGC 2703
Db 4046 ACAGAAAGTGAAGGTTGTCCAGAGGCCCTGGACAAAGCCAGAGAGGCCGACCTGC 4105
Qy 2704 CTAGTGTCTACTCAGGCTCTCTGCAATTCAGAACCGAGATTTGATGTTCTCTCAC 2763
Db 4106 ATTGTGATTGCTACCGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAG 4165
Qy 2764 AATCGAAGATAAGGACAGAGGAACTCATCAAGGCTCCGTGAGAAATCCGAGACATAT 2823


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QY 2401 ATTGCTGAGAACATGCGCTATGTTGATGACACAGCCGTTGGTGGCCATTAGATGATCAAA 2460
DB |||||
QY 2401 ATTGCTGAGAACATGCGCTATGTTGATCAACAGCCGTTGGTGGCCATTAGATGATCAAA 2460
DB |||||
QY 2461 GAAGCCGCAAAATGAGCAAAATATCCATCTCTTTTATTGAAGGTTCTCCCTCAGAAATCAAC 2520
DB |||||
QY 2461 GAAGCCGCAAAATGAGCAAAATATCCATCTCTTTTATTGAAGGTTCTCCCTCAGAAATCAAC 2520
DB |||||
QY 2521 ACAATAGTTGGAGTGAAGAGGACACAGCTTTCTGGCGGCAGAAAACAAGACTAGCTATT 2580
DB |||||
QY 2521 ACAATAGTTGGAGTGAAGAGGACACAGCTTTCTGGCGGCAGAAAACAAGACTAGCTATT 2580
DB |||||
QY 2581 GCAAGGCTCTCTCCAAACCAAAATTTATTTGTTGATGAGGACCACTTCAGCCCTC 2640
DB |||||
QY 2581 GCAAGGCTCTCTCCAAACCAAAATTTATTTGTTGATGAGGACCACTTCAGCCCTC 2640
DB |||||
QY 2641 GATAATGACAGTGAAGAGGACACAGCTTTCTGGCGGCAGAAAACAAGACTAGCTATT 2700
DB |||||
QY 2641 GATAATGACAGTGAAGAGGAGTGTTCAGCATGCCCTTGATAAAGCCAGGACGGAGGACA 2700
DB |||||
QY 2701 TGCTAGTGTCACTCAGAGGCTCTCTGCAATTCAGACGCGAGTTGATGTTCTG 2760
DB |||||
QY 2701 TGCTAGTGTCACTCAGAGGCTCTCTGCAATTCAGACGCGAGTTGATGTTCTG 2760
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QY 2761 CACAATGGAAGATAAAGGAACAAGGAACCTCATCAAGAGCTCTCGAGAAATCGAGACATA 2820
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QY 2761 CACAATGGAAGATAAAGGAACAAGGAACCTCATCAAGAGCTCTCGAGAAATCGAGACATA 2820
DB |||||
QY 2821 TATTTTAAAGTGTAGTGAATGCAGTGCAGTGA 2856
DB |||||
QY 2821 TATTTTAAAGTGTAGTGAATGCAGTGCAGTGA 2856
DB |||||

RESULT 2
US-09-873-409-12
; Sequence 12, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayed, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 3177
; TYPES: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1
; LOCATION: (198)..(198)
; OTHER INFORMATION: n at position 198 represents any nucleotide (A, T, C or G)
US-09-873-409-12

Query Match 94.2%; Score 2690.6; DB 9; Length 3177;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 160 TCCTCATATTGATGAAGAACCCAGTATAGATACTTTTCCACAGCTCGATATAAACCT 219
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QY 481 TTCAGGTTATTGGAAGAAACCCAGTATAGATACTTTTCCACAGCTCGATATAAACCT 540
DB |||||
QY 220 GAATCCATAGAAGAACTGGGAATTTAAATTTCTTTCAATTTATCCATCAAGACCA 279
DB |||||
QY 541 GAATCCATAGAAGAACTGGGAATTTAAATTTCTTTCAATTTATCCATCAAGACCA 600
DB |||||
QY 280 TCTATCAGATTTGGAAGGCTGATCTCAGATTTAGCTGGAGAGACAGTCCGCTTG 339
DB |||||
QY 601 TCTATCAGATTTGGAAGGCTGATCTCAGATTTAGCTGGAGAGACAGTCCGCTTG 660
DB |||||

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QY 340 GTCCGCTCTCAATGGCAGTGGGAAGAGTAGCGTAGTCCAGCTTCTCGAGAGGTTATATGAT 399
DB |||||
QY 661 GTCCGCTCTCAATGGCAGTGGGAAGAGTAGCGTAGTCCAGCTTCTCGAGAGGTTATATGAT 720
DB |||||
QY 400 CCGGATGATGGCTTTATCATGGTGGATGAGAAATGACATCAGAGCTTTAAATGTGGGCAAT 459
DB |||||
QY 721 CCGGATGATGGCTTTATCATGGTGGATGAGAAATGACATCAGAGCTTTAAATGTGGGCAAT 780
DB |||||
QY 460 TATCAGAGCCATATTTGGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCAATCATGAT 519
DB |||||
QY 781 TATCAGAGCCATATTTGGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCAATCATGAT 840
DB |||||
QY 520 AACCAATATCAAGTATGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 579
DB |||||
QY 841 AACCAATATCAAGTATGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB |||||
QY 580 GAAGCAAAATGCGTATGATTTTATCATGAGTTCCTTAATAAATTTAATCAATGTTAGG 639
DB |||||
QY 901 GAAGCAAAATGCGTATGATTTTATCATGAGTTCCTTAATAAATTTAATCAATGTTAGG 960
DB |||||
QY 640 GAAGCAAAATGCGTATGATTTTATCATGAGTTCCTTAATAAATTTAATCAATGTTAGG 699
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QY 961 GAAGCAAAATGCGTATGATTTTATCATGAGTTCCTTAATAAATTTAATCAATGTTAGG 1020
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QY 700 GTTCCGAAACCCCAAGTATCTGATTTTAGATGAGGCTAGCTCTGCCCTGGATTCAGAAAGC 759
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QY 1021 GTTCCGAAACCCCAAGTATCTGATTTTAGATGAGGCTAGCTCTGCCCTGGATTCAGAAAGC 1080
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QY 760 AAGTCAGCTGTTCAAGCTGCACTGGAGAAAGGCGAGCAAAAGTGGGACTACATCAATTCGTTA 819
DB |||||
QY 1081 AAGTCAGCTGTTCAAGCTGCACTGGAGAAAGGCGAGCAAAAGTGGGACTACATCAATTCGTTA 1140
DB |||||
QY 820 GCACACCCACTTCTATTTTGAAGTGCAGATTTGATTTGACCCCTAAAGGATGGAATG 879
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QY 1141 GCACACCCACTTCTATTTTGAAGTGCAGATTTGATTTGACCCCTAAAGGATGGAATG 1200
DB |||||
QY 880 CTGGCGGAGAAAGGAGGACATCTGAACTTAATGCAAAAGGAGGCTGATTTATTTCACTT 939
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QY 1201 CTGGCGGAGAAAGGAGGACATCTGAACTTAATGCAAAAGGAGGCTGATTTATTTCACTT 1260
DB |||||
QY 940 GTGATGTCACAGGATATTTAAAGGCTGATGAACAGATGAGTCAATCAATCAATTTCTACT 999
DB |||||
QY 1261 GTGATGTCACAGGATATTTAAAGGCTGATGAACAGATGAGTCAATCAATCAATTTCTACT 1320
DB |||||
QY 1000 GAAGAAAGACCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1059
DB |||||
QY 1321 GAAGAAAGACCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
DB |||||
QY 1060 GACAGGCTGAGGATCCACCCCACTTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1119
DB |||||
QY 1381 GACAGGCTGAGGATCCACCCCACTTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1440
DB |||||
QY 1120 AAAATTTTAAAGTTAAACCAAGCTGAATGGCTTTTGTGGTTCTGGGACATTTGGCTTCT 1179
DB |||||
QY 1441 AAAATTTTAAAGTTAAACCAAGCTGAATGGCTTTTGTGGTTCTGGGACATTTGGCTTCT 1500
DB |||||
QY 1180 GTTCTAAATGGAACGTGTTTCAATCCAGTATTTTCAATCCAGTATTTTCAATCCAGTATTT 1239
DB |||||
QY 1501 GTTCTAAATGGAACGTGTTTCAATCCAGTATTTTCAATCCAGTATTTTCAATCCAGTATTT 1560
DB |||||
QY 1240 TTTGAAATTAATGATTAATAACCAATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1299
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QY 1561 TTTGAAATTAATGATTAATAACCAATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1620
DB |||||
QY 1300 GTCAATTTTGGTGTATTTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1359
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QY 1621 GTCAATTTTGGTGTATTTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
DB |||||
QY 1360 GCAGGGGAAATTTTAAACGATGAGATTAAGAGACTTTGGCTTTCAAGGCTGATTTATATCAG 1419
DB |||||
QY 1681 GCAGGGGAAATTTTAAACGATGAGATTAAGAGACTTTGGCTTTCAAGGCTGATTTATATCAG 1740
DB |||||

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Qy	1420	GATATTGCCCTGGTTTGTATGAAAGAGAAAA	CAGCACAGGAGCGCTTGTACAACAATATTAGCC	1479
Db	1741	GATAATTGCCCTGGTTTGTATGAAAGAGAAAA	CAGCACAGGAGCGCTTGTACAACAATATTAGCC	1800
Qy	1480	ATAGATATAGCACAAATTC	CAAGGAGCAACAGGTTCCAGGATTCGCGCTCTTAAACACAAAT	1539
Db	1801	ATAGATATAGCACAAATTC	CAAGGAGCAACAGGTTCCAGGATTCGCGCTCTTAAACACAAAT	1860
Qy	1540	GCAACTAACATGGGACCTTT	CAGTTATCAATTTCCCTTTATATATGATGGAGATGACATTC	1599
Db	1861	GCAACTAACATGGGACCTTT	CAGTTATCAATTTCCCTTTATATATGATGGAGATGACATTC	1920
Qy	1600	CTGATCTGTGATATGCTCCAGTACTTC	CGCTGCACAGGATGATGAAACCGCAGCAATG	1659
Db	1921	CTGATCTGTGATATGCTCCAGTACTTC	CGCTGCACAGGATGATGAAACCGCAGCAATG	1980
Qy	1660	ACTGGATTTGCCAACAAAGATAAGCAAGAACTT	AAAGCATCTCGAAGATAGCAACTGAA	1719
Db	1981	ACTGGATTTGCCAACAAAGATAAGCAAGAACTT	AAAGCATCTCGAAGATAGCAACTGAA	2040
Qy	1720	GCTTTGGAGATATATACGTACTATAGTCTCATTA	CAAGGGAAAAAGCCCTCGAGCAAAATG	1779
Db	2041	GCTTTGGAGATATATACGTACTATAGTCTCATTA	CAAGGGAAAAAGCCCTCGAGCAAAATG	2100
Qy	1780	TATGAAGAGATGCTTTCAGACTCAACACAGAAAACT	CTCGAAGAAAGACACAGATATTGGA	1839
Db	2101	TATGAAGAGATGCTTTCAGACTCAACACAGAAAACT	CTCGAAGAAAGACACAGATATTGGA	2160
Qy	1840	AGCTGTTATGCAATTCAGCCATG	CCCTTTATATATTTTGCCTATGACAGAGGTTTCGATTT	1899
Db	2161	AGCTGTTATGCAATTCAGCCATG	CCCTTTATATATTTTGCCTATGACAGAGGTTTCGATTT	2220
Qy	1900	GGAGCCTATTTAATTC	CAAGCTGGACGATGACCCAGAGGCGCATGTTCAATAGTTTTTACT	1959
Db	2221	GGAGCCTATTTAATTC	CAAGCTGGACGATGACCCAGAGGCGCATGTTCAATAGTTTTTACT	2280
Qy	1960	GCAATTCGATATGGAGCTATGGCCATCGGAAAAAC	CGTTCGTTTGGCTCTCGAATATTC	2019
Db	2281	GCAATTCGATATGGAGCTATGGCCATCGGAAAAAC	CGTTCGTTTGGCTCTCGAATATTC	2340
Qy	2020	AAAGCCAAATCGGGGCTGGCGATCTCTGTTGCCTT	GTTCGAAAGAACCAATATAGAC	2079
Db	2341	AAAGCCAAATCGGGGCTGGCGATCTCTGTTGCCTT	GTTCGAAAGAACCAATATAGAC	2400
Qy	2080	AGCGCAGTCAAGAGGAAAAAGCCAGACACATGTC	CAAGGGAATTTAGAGTTTCAGAA	2139
Db	2401	AGCGCAGTCAAGAGGAAAAAGCCAGACACATGTC	CAAGGGAATTTAGAGTTTCAGAA	2460
Qy	2140	GTCTCTTTCTTATTCANGTGCGCCAGATGTTTT	GTATCTCTCGTGCTTATCCCTCAGT	2199
Db	2461	GTCTCTTTCTTATTCANGTGCGCCAGATGTTTT	GTATCTCTCGTGCTTATCCCTCAGT	2520
Qy	2200	ATTGAGCGAGAAAGACAGTAGCATTTGTGGGGAG	CAGCGCTGTGGAAAAAGCATCT	2259
Db	2521	ATTGAGCGAGAAAGACAGTAGCATTTGTGGGGAG	CAGCGCTGTGGAAAAAGCATCT	2580
Qy	2260	GTTCAACTTCTGCAGAGCTTTATGACCCCGTGA	AGGACAAAGTCGTTTGATGPGTGTG	2319
Db	2581	GTTCAACTTCTGCAGAGCTTTATGACCCCGTGA	AGGACAAAGTCGTTTGATGPGTGTG	2640
Qy	2320	GATGCAAAAGATTTGAATGATACGTGCTCGTTC	CGAATAGCAATCGTCTCTCAAGAG	2379
Db	2641	GATGCAAAAGATTTGAATGATACGTGCTCGTTC	CGAATAGCAATCGTCTCTCAAGAG	2700
Qy	2380	CCTGTGCTCTTCAACTG	CAGCATTTGCTGAGAACATCGCCTATGGTGACAAAGCCGPGTGTG	2439
Db	2701	CCTGTGCTCTTCAACTG	CAGCATTTGCTGAGAACATCGCCTATGGTGACAAAGCCGPGTGTG	2760
Qy	2440	GTGCCATTAGATGAGATCAAAAGACCGCAATG	CGCAATATCCATCTTTTATTGAA	2499
Db	2761	GTGCCATTAGATGAGATCAAAAGACCGCAATG	CGCAATATCCATCTTTTATTGAA	2820
Qy	2500	GTCTCTCCCTGAGAAATACAAACACAAAGTTG	GAATCTGAAAGAGACACAGCTTTCTGTGCGCGC	2559

Db	2821	GGTCTCCTCGAAGAAATACAAACACACAAAGTTGGACTGAAGGACACAGCTTCTCGCGGC	2880
Qy	2560	CAGAAACAAGA CTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAAATTTTATTGTTG	2619
Db	2881	CAGAAACAAGACTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAAATTTTATTGTTG	2940
Qy	2620	GATGAGGCCACTTTCAGCCCTCGATAATGACAGTGAAGAGTGTTTCAGCATGCCCTTGAT	2679
Db	2941	GATGAGGCCACTTTCAGCCCTCGATAATGACAGTGAAGAGTGTTTCAGCATGCCCTTGAT	3000
Qy	2680	AAAGCCAGGACGGGAAGGACATSCCTTAGTGGTCACCTCAGAGGCTCTCTGCAATTCAGAAC	2739
Db	3001	AAAGCCAGGACGGGAAGGACATSCCTTAGTGGTCACCTCAGAGGCTCTCTGCAATTCAGAAC	3060
Qy	2740	GCAGATTGATAGTGGTCTGCAATGGAAGATAAAGGACACAGGACTCATCAAGAG	2799
Db	3061	GCAGATTGATAGTGGTCTGCAATGGAAGATAAAGGACACAGGACTCATCAAGAG	3120
Qy	2800	CTCCTGAGAAATCGAGACATATATTTTAAGTTAGTGAATGCCACAGTCAGTCAGTGA	2856
Db	3121	CTCCTGAGAAATCGAGACATATATTTTAAGTTAGTGAATGCCACAGTCAGTCAGTGA	3177

RESULT 3

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RESULT 3
US-09-873-409-14
? Sequence 14: Application US/09873409
? Patent No. US20020037522A1
? GENERAL INFORMATION:
? APPLICANT: Frank, Markus
? APPLICANT: Sayegh, Mohamed
? TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
? TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
? FILE REFERENCE: #1994/268611
? CURRENT APPLICATION NUMBER: US/09/873,409
? CURRENT FILING DATE: 2001-06-05
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 14
? LENGTH: 3621
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-873-409-14

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Query Match	94.2%	Score 2690.6;	DB 9;	Length 3621;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2693;	Conservative	0;	Mismatches	4;
			Indels	0;
			Gaps	0;

Qy	160	TCCCTCATTAATGATATAGAAACCCAGATATAGATAACTTTTCCACAGCTGATATAAACCT	2119
Db	925	TTCCAGGTATTGATAAGAAACCCAGATATAGATAACTTTTCCACAGCTGATATAAACCT	984
Qy	220	GAATCCCATAGAGGAACTGTGGAAATTAAATAATGTTCTTTTCAATTATCCATCAAGACCA	279
Db	985	GAATCCCATAGAGGAACTGTGGAAATTAAATAATGTTCTTTTCAATTATCCATCAAGACCA	1044
Qy	280	TCTATCAAGATCTCGAAGATCTCGAATCTCAGAAATTAAGTCTGAGAGACAGTCGCCCTTG	339
Db	1045	TCTATCAAGATCTCGAAGATCTCGAATCTCAGAAATTAAGTCTGAGAGACAGTCGCCCTTG	1104
Qy	340	GTCGGTCTTCAATGSCATCTGGGAGAGATACGGTATGATCCAGCTTCTGCGAGAGTTATATGAT	399
Db	1105	GTCGGTCTTCAATGSCATCTGGGAGAGATACGGTATGATCCAGCTTCTGCGAGAGTTATATGAT	1164
Qy	400	CCGGAATGATGGCTTTATCATGGTGCATGAGAATGACATCAGAGCTTTTAAATGTGCGGCAT	459
Db	1165	CCGGAATGATGGCTTTATCATGGTGCATGAGAATGACATCAGAGCTTTTAAATGTGCGGCAT	1224
Qy	460	TATCGAGACCATATTGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCAACCATCAGT	519
Db	1225	TATCGAGACCATATTGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCAACCATCAGT	1284
Qy	520	AACAAATATCAAGTATGGAACGAGATGATGTGACTGATGAAGAGATGGAGAGAGCAGCAAGG	579

2365	CTGATTCTGAGTATTGCTCCAGTACTGCGGTGACAGGAAATGATTTGAAACCGCAGCAATG	2422
1660	ACTGGATTTGCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTTGGAAAGATAGCAACTGAA	1719
2425	ACTGGATTTGCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTTGGAAAGATAGCAACTGAA	2484
1720	GCATTTGGAGATATACGTACTATATGTGTCATTAAACAAGGGAAGAAAGCCCTTCGAGCAAAATG	1779
2485	GCATTTGGAGATATACGTACTATATGTGTCATTAAACAAGGGAAGAAAGCCCTTCGAGCAAAATG	2544
1780	TATGAAGAGATCCTTCAGACTCAACACAGAAATACCTCGAAGAAAGCACAGATTATTGGA	1839
2545	TATGAAGAGATCCTTCAGACTCAACACAGAAATACCTCGAAGAAAGCACAGATTATTGGA	2604
1840	AGCTGTATTGCAATTCAGCCATCGCTTATATATTTTGCCTATGCGACAGGGTTTCGATTT	1899
2605	AGCTGTATTGCAATTCAGCCATCGCTTATATATTTTGCCTATGCGACAGGGTTTCGATTT	2664
1900	GGAGCCTATTAAATTCAGCTGGAGGAATGACCCAGAGGGGCATGTTTCAATAGTTTTTACT	1959
2665	GGAGCCTATTAAATTCAGCTGGAGGAATGACCCAGAGGGGCATGTTTCAATAGTTTTTACT	2724
1960	GCAATTCGATATGGAGCTATAGCCATTCGGAAACAGCTCGCTTTTGGCTCCTGTAATTTCC	2019
2725	GCAATTCGATATGGAGCTATAGCCATTCGGAAACAGCTCGCTTTTGGCTCCTGTAATTTCC	2784
2020	AAAGCCAAATTCGGGGCTCGGCATCTGTTTGGCTTGTTCGAAAAAGAAACAAATATAGAC	2079
2785	AAAGCCAAATTCGGGGCTCGGCATCTGTTTGGCTTGTTCGAAAAAGAAACAAATATAGAC	2844
2080	AGCCGAGTCAAGAAAGGGAACAGACATCTGAAGGGAATTTAGAGTTTCAGAGAA	2139
2845	AGCCGAGTCAAGAAAGGGAACAGACATCTGAAGGGAATTTAGAGTTTCAGAGAA	2904
2140	GTCTCTTCTTCTATNCATGTCGCCCCAGATGTTTTTCATCTCCGTGGCTTATCCCTCAGT	2199
2905	GTCTCTTCTTCTATNCATGTCGCCCCAGATGTTTTTCATCTCCGTGGCTTATCCCTCAGT	2964
2200	ATTGAGCGAGAAAGACAGTAGTACATTTGTGGGAGCAGCGGCTGTGGGAAAGCACTTCT	2259
2965	ATTGAGCGAGAAAGACAGTAGTACATTTGTGGGAGCAGCGGCTGTGGGAAAGCACTTCT	3024
2260	GTTCACATTTCTCAGACATTTATGACCCCGTGCAGAGCACAGTCTGTTTCATGGTGG	2319
3025	GTTCACATTTCTCAGACATTTATGACCCCGTGCAGAGCACAGTCTGTTTCATGGTGG	3084
2320	GATGCAAAAGAAATTCGAATGACAGTGGCTCCGTTCCCAAATAGCAATCGTTCCTCAAGAG	2379
3085	GATGCAAAAGAAATTCGAATGACAGTGGCTCCGTTCCCAAATAGCAATCGTTCCTCAAGAG	3144
2380	CCTGTGCTTCTCACTGCAGCAATGCTGAGAAACATCGGCTATGGTGTGAACAAGCCGTGG	2439
3145	CCTGTGCTTCTCACTGCAGCAATGCTGAGAAACATCGGCTATGGTGTGAACAAGCCGTGG	3204
2440	GTGCCATTATAGTAGATCAAGAAGCCCAATGACGAAATPATCCATTCTTTTATTTGAA	2499
3205	GTGCCATTATAGTAGATCAAGAAGCCCAATGACGAAATPATCCATTCTTTTATTTGAA	3264
2500	GGTCTCCCTGAGAAATACAACAACAAGTTGCACTGAAAGGAGCAAGCTTTCTGCGCGC	2559
3265	GGTCTCCCTGAGAAATACAACAACAAGTTGCACTGAAAGGAGCAAGCTTTCTGCGCGC	3324
2560	CAGAAACAAAGACTAGCTATTTCGAGGGCTCTTCTCCAAAACCCAAAATTTTATTTGTTG	2619
3325	CAGAAACAAAGACTAGCTATTTCGAGGGCTCTTCTCCAAAACCCAAAATTTTATTTGTTG	3384
2620	GATGAGGCCACTTTCAGCCCTCGATTAATGACAGTGTGAGAGGTGGTTTCAGCATGCCCTTGAT	2679
3385	GATGAGGCCACTTTCAGCCCTCGATTAATGACAGTGTGAGAGGTGGTTTCAGCATGCCCTTGAT	3444
2680	AAAGCCAGGACGGGAAGGACATGCTAGTGGTCACTCAGAGCTCTCTGCANTTCAGAC	2739
3445	AAAGCCAGGACGGGAAGGACATGCTAGTGGTCACTCAGAGCTCTCTGCANTTCAGAC	3504

QY 2740 GCAGATTGATAGTGGTCTGACAAATGGAAGATGAAGGAAACAGGAACTCATCAAGAG 2799
DB 3505 GCAGATTGATAGTGGTCTGACAAATGGAAGATGAAGGAAACAGGAACTCATCAAGAG 3564
QY 2800 CTCCTGAGAAATCGAGACATATATTTAAAGTTAGTGAATGACATGAGTCAAGTGA 2856
DB 3565 CTCCTGAGAAATCGAGACATATATTTAAAGTTAGTGAATGACATGAGTCAAGTGA 3621

RESULT 4
US-09-873-409-13
; Sequence 13, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 3702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1
; LOCATION: (723)...(723)
; OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)

US-09-873-409-13

Query Match 94.2%; Score 2690.6; DB 9; Length 3702;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 160 TCCCTCATTTATGATAAGAAACCCAGTATAGATAACTTTTCCACAGCTGGATATAAACCT 219
DB 1006 TCCAGGTATTTGATAAGAAACCCAGTATAGATAACTTTTCCACAGCTGGATATAAACCT 1065

QY 220 GAATCCATAGAGGAACTGTGAATTTAAATGTTCTTCAATATCCATCAAGACCA 279
DB 1066 GAATCCATAGAGGAACTGTGAATTTAAATGTTCTTCAATATCCATCAAGACCA 1125

QY 280 TCTATCAAGATTTCTGAAGGTTCTGAATCTCAGAAATTAAGTCTGGAGACAGTGGCCTTG 339
DB 1126 TCTATCAAGATTTCTGAAGGTTCTGAATCTCAGAAATTAAGTCTGGAGACAGTGGCCTTG 1185

QY 340 GTCCGTCTCAATGCGAGTGGGAAGATGACGTAGTCCAGCTTCTCCAGAGGTTATATGAT 399
DB 1186 GTCCGTCTCAATGCGAGTGGGAAGATGACGTAGTCCAGCTTCTCCAGAGGTTATATGAT 1245

QY 400 CCGGATGATGGCTTTTATCATGTTGGATGAGATGACATCAGAGCTTTAAATGTGGCGCAT 459
DB 1246 CCGGATGATGGCTTTTATCATGTTGGATGAGATGACATCAGAGCTTTAAATGTGGCGCAT 1305

QY 460 TATCGAGACCATATTTGGAGTGTATGATGAGAGCTTTTGTGGGACCAACATCAGT 519
DB 1306 TATCGAGACCATATTTGGAGTGTATGATGAGAGCTTTTGTGGGACCAACATCAGT 1365

QY 520 AACAAATATCAAGTATGCGAGATGATGACTGATGAAGAGATGAGAGAGGACGACGAGG 579
DB 1366 AACAAATATCAAGTATGCGAGATGATGACTGATGAAGAGATGAGAGAGGACGACGAGG 1425

QY 580 GAAGCAATGCGTATGATTTTATCATGAGGTTTCTTAATAATTAATATGATGAGG 639
DB 1426 GAAGCAATGCGTATGATTTTATCATGAGGTTTCTTAATAATTAATATGATGAGG 1485

QY 640 GAAAGAGGCTCAATGAGTGGGCGAGGACGAGGATGCGAATGCTCGTGCCTTA 699
DB 1486 GAAAGAGGCTCAATGAGTGGGCGAGGACGAGGATGCGAATGCTCGTGCCTTA 1545

QY 700 GTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGCTCCCTGGATTCAGAAAGC 759
DB 1546 GTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGCTCCCTGGATTCAGAAAGC 1605

QY 760 AAGTCAGCTGTTCAAGCTGCACTGGAGAGCCAGCAAGAGTGGACTACAAATCGTGTA 819
DB 1506 AAGTCAGCTGTTCAAGCTGCACTGGAGAGCCAGCAAGAGTGGACTACAAATCGTGTA 1665

QY 820 GCACACCGACTTTTCTACTATTGGAAGTGCAGATTTGATGACCTCCCTAAAGATGGAATG 879
DB 1666 GCACACCGACTTTTCTACTATTGGAAGTGCAGATTTGATGACCTCCCTAAAGATGGAATG 1725

QY 880 CTGGCGGAGAAAGGAGGACACATGCTGAACTAATGCAAAAGAGAGTCTATATATTACCTT 939
DB 1726 CTGGCGGAGAAAGGAGGACACATGCTGAACTAATGCAAAAGAGAGTCTATATATTACCTT 1785

QY 940 GTGATGTCACAGGATATTAATAAAGCTGATGAACAGATGAGTCAAGATATTTCTACT 999
DB 1786 GTGATGTCACAGGATATTAATAAAGCTGATGAACAGATGAGTCAAGATATTTCTACT 1845

QY 1000 GAAAGAAAGACCAACTCACCTTCCTGCACTCTGTGGAAGAGCATCAAGTCAGACTTCATT 1059
DB 1846 GAAAGAAAGACCAACTCACCTTCCTGCACTCTGTGGAAGAGCATCAAGTCAGACTTCATT 1905

QY 1060 GACAAGGCTGAGGAATCCACCCTAATCTAAAGAGATAAGTCTTCTGAAAGTCTCTCTATTA 1119
DB 1906 GACAAGGCTGAGGAATCCACCCTAATCTAAAGAGATAAGTCTTCTGAAAGTCTCTCTATTA 1965

QY 1120 AATAATTTAAAGTTAAACAGCCCTGATGCGCTTTGTTGTTCTGGGAGCAATGGCTTCT 1179
DB 1966 AATAATTTAAAGTTAAACAGCCCTGATGCGCTTTGTTGTTCTGGGAGCAATGGCTTCT 2025

QY 1180 GTTCTAAATGGAATCTGTTCAATCCAGTATTTTCCATCATCTTTTCCAAAAATTAACCATG 1239
DB 2026 GTTCTAAATGGAATCTGTTCAATCCAGTATTTTCCATCATCTTTTCCAAAAATTAACCATG 2085

QY 1240 TTTGGAATAATGATAAAACCAATTAAGCATGATGCGAAATTTATTTCCATGATATTC 1299
DB 2086 TTTGGAATAATGATAAAACCAATTAAGCATGATGCGAAATTTATTTCCATGATATTC 2145

QY 1300 GTCAATTTGGGTGTATTTGCTTTGTGCTATTTTCAATGAGGATTTATTTTACGCGCAGA 1359
DB 2146 GTCAATTTGGGTGTATTTGCTTTGTGCTATTTTCAATGAGGATTTATTTTACGCGCAGA 2205

QY 1360 GCAGGGAAATTTTAAAGATGAGATTAAGACACTTGGCTTCCAAAGCCATGTTATATCAG 1419
DB 2206 GCAGGGAAATTTTAAAGATGAGATTAAGACACTTGGCTTCCAAAGCCATGTTATATCAG 2265

QY 1420 GATATTCCTGCTGTTGATGAAAGGAAACAGACAGGAGGCTTGACAAATATTAGCC 1479
DB 2266 GATATTCCTGCTGTTGATGAAAGGAAACAGACAGGAGGCTTGACAAATATTAGCC 2325

QY 1480 ATAGATATAGCACAAATTTCAAGGAGCAACAGGTTCCAGGATTTGGCGTTTAAACACAAAT 1539
DB 2326 ATAGATATAGCACAAATTTCAAGGAGCAACAGGTTCCAGGATTTGGCGTTTAAACACAAAT 2385

QY 1540 GCAACTAAATGAGGACTTTTCAAGTATGATTTCTTTTATATGATGAGGAGATGACATTC 1599
DB 2386 GCAACTAAATGAGGACTTTTCAAGTATGATTTCTTTTATATGATGAGGAGATGACATTC 2445

QY 1600 CTGATTCAGTATTTGCTCCAGTACTTGGCTGACAGGATGATTTGAAACCGCAGCAATG 1659
DB 2446 CTGATTCAGTATTTGCTCCAGTACTTGGCTGACAGGATGATTTGAAACCGCAGCAATG 2505

QY 1660 ACTGATTTCCGAAACAAAGATAGCAAGATTTAAGCATGCTGGAAGATGAGCACTGAA 1719
DB 2506 ACTGATTTCCGAAACAAAGATAGCAAGATTTAAGCATGCTGGAAGATGAGCACTGAA 2565

QY 1720 GCTTTGGAGATATACGTAATGATGATGATTAAGGAGGAAAGGCTTCGAGGCAATG 1779
DB 2566 GCTTTGGAGATATACGTAATGATGATGATTAAGGAGGAAAGGCTTCGAGGCAATG 2625

Qy	460	TATCGAGACCAATATTTGGAGTGGTTAGTCAAGAGCCTCTTTTGTTCGGGACCAACATCAGT	519
Db	1381	TATCGAGACCAATATTTGGAGTGGTTAGTCAAGAGCCTCTTTTGTTCGGGACCAACATCAGT	1440
Qy	520	AACAATATCAAGTATGCACGAGATGATGTGACTGATCAAGAGATGGAGAGCAGCAAGG	579
Db	1441	AACAATATCAAGTATGCACGAGATGATGTGACTGATCAAGAGATGGAGAGCAGCAAGG	1500
Qy	580	GAAGCAAAATGCGTATGATTTTATCATCGAGGTTTCCTTAATAAAATTTAATAATTTGGTAGGG	639
Db	1501	GAAGCAAAATGCGTATGATTTTATCATCGAGGTTTCCTTAATAAAATTTAATAATTTGGTAGGG	1560
Qy	640	GAATAAGGAGCTCAAAATGAGTGGAGGCGCAAGAAACAGAGGATCGCAATGCTGCTGCTTAA	699
Db	1561	GAATAAGGAGCTCAAAATGAGTGGAGGCGCAAGAAACAGAGGATCGCAATGCTGCTGCTTAA	1620
Qy	700	GTTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGTCTGCCCTGGATTCAGAAAGC	759
Db	1621	GTTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGTCTGCCCTGGATTCAGAAAGC	1680
Qy	760	AAGTCAGCTGTTCAAGCTGCACCTGGAGAGCGCAGCAAGGTCGGACTCAANTCGTGGTA	819
Db	1681	AAGTCAGCTGTTCAAGCTGCACCTGGAGAGCGCAGCAAGGTCGGACTCAANTCGTGGTA	1740
Qy	820	GCACACCGACTTCTACTATTTCGAAGTGCAGATTTGATTTGACCCCTAAAGGATGGAATG	879
Db	1741	GCACACCGACTTCTACTATTTCGAAGTGCAGATTTGATTTGACCCCTAAAGGATGGAATG	1800
Qy	880	CTGCGGAGAAAGAGACACATGCTGAACTAATGGCAAAAACGAGGTCTATATTTACATT	939
Db	1801	CTGCGGAGAAAGAGACACATGCTGAACTAATGGCAAAAACGAGGTCTATATTTACATT	1860
Qy	940	GTGATGTCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTTCTACT	999
Db	1861	GTGATGTCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTTCTACT	1920
Qy	1000	GAAGAAGACCAACTCACTTCCTCTGCACCTCTGTGAAGAGCATCAAGTCAGACTTCATT	1059
Db	1921	GAAGAAGACCAACTCACTTCCTCTGCACCTCTGTGAAGAGCATCAAGTCAGACTTCATT	1980
Qy	1060	GACAAGGCTGAGGAATCCACCCCAATCTAAAGAGATAAGTCTCTCTGAAGTCTCTCTATTAA	1119
Db	1981	GACAAGGCTGAGGAATCCACCCCAATCTAAAGAGATAAGTCTCTCTGAAGTCTCTCTATTAA	2040
Qy	1120	AAAAATTTAAAGTTAAACAAAGCCTGAAATGCCCTTTTGTGTTCTGGGACATATGGCTTCT	1179
Db	2041	AAAAATTTAAAGTTAAACAAAGCCTGAAATGCCCTTTTGTGTTCTGGGACATATGGCTTCT	2100
Qy	1180	GTTCTTAATGGAATGCTGATCCAGTATTTTCCATCATCTTTCGCAAAAATTAATACCATG	1239
Db	2101	GTTCTTAATGGAATGCTGATCCAGTATTTTCCATCATCTTTCGCAAAAATTAATACCATG	2160
Qy	1240	TTTTCGAAATTAATGATAAAACCAATTAAAGCATGATCCAGAAATTTATTCATGATATTC	1299
Db	2161	TTTTCGAAATTAATGATAAAACCAATTAAAGCATGATCCAGAAATTTATTCATGATATTC	2220
Qy	1300	GTCAATTTTGGTGTTATTTGCTTTGTCAGTTATTTTATGTCAGGGAATTTTTCAGGCGAGA	1359
Db	2221	GTCAATTTTGGTGTTATTTGCTTTGTCAGTTATTTTATGTCAGGGAATTTTTCAGGCGAGA	2259
Qy	1360	GCAGGGGAAAATTTTAAACGATGAGATTAAGACACTTTGGCCTTTCAAAGCCATGTTATATCAG	1419
Db	2260	GCAGGGGAAAATTTTAAACGATGAGATTAAGACACTTTGGCCTTTCAAAGCCATGTTATATCAG	2262
Qy	1420	GATATTCCTGGTTTGAATGAATAAGGAAAAACAGCACAGGAGCTTGACAAACAATATTAGCC	1479
Db	2263	GATATTCCTGGTTTGAATGAATAAGGAAAAACAGCACAGGAGCTTGACAAACAATATTAGCC	2322
Qy	1480	ATAGATATAGCACAAATTTCAAGGAGACACAGGTTTCCAGGATTCGCTCTTAAACACAAAT	1539
Db	2323	ATAGATATAGCACAAATTTCAAGGAGACACAGGTTTCCAGGATTCGCTCTTAAACACAAAT	2382
Qy	1540	GCAACTAACATGGGACTTTCAGTTATCATTTTCTTTTATATATGATGATGGGAGATGCAATTC	1599

2383	Db		GCACCTAA	CATGGGACTTT	CGATTAT	CAATTCCTTTATATATGATGGGAGATGACATTC	2442
1600	Qy	CTGATTC	TCAGTAT	TGCTTC	CAGTACTT	CGCGTGACACAGGAATGATGAAACCGCAGCAATG	1659
2443	Db	CTGATTC	TCAGTAT	TGCTTC	CCAGTACT	TGCGGTGCACAGGAATGATGAAACCGCAGCAATG	2502
1660	Qy	ACTGGATTTCC	CAACAAAGATTA	ACGAAGAACTT	TAAGTAGCTCTGGAAGATAGCAACTGAA	1719	
2503	Db	ACTGGATTTCC	CAACAAAGATTA	ACGAAGAACTT	TAAGTAGCTCTGGAAGATAGCAACTGAA	2562	
1720	Qy	GCCTTTGGAGAA	TATACGTACTAT	AGTAGTGTCA	TAAACAGGAAAAAGCCITTCGAGCAAAATG	1779	
2563	Db	GCCTTTGGAGAA	TATACGTACTAT	AGTAGTGTCA	TAAACAGGAAAAAGCCITTCGAGCAAAATG	2622	
1780	Qy	TATGAAGAGATGCTT	CAGACTCA	ACACAGAAATAC	CTCGAAGAAAAACACAGATNTTGGAA	1839	
2623	Db	TATGAAGAGATGCTT	CAGACTCA	ACACAGAAATAC	CTCGAAGAAAAACACAGATNTTGGAA	2682	
1840	Qy	AGCTGTTTATGCATTT	CAGCCATG	CGTTTATATATTTT	TGCTCTATGACAGAGGGTTTCGATTT	1899	
2683	Db	AGCTGTTTATGCATTT	CAGCCATG	CGTTTATATATTTT	TGCTCTATGCGCAGAGGGTTTCGATTT	2742	
1900	Qy	GGAGCCTATT	TTAATCAAGCT	TGACGAGTAG	CCCCAGAGGGCAATGTTTCATAGTTTTTACT	1959	
2743	Db	GGAGCCTATT	TTAATCAAGCT	TGACGAGTAG	CCCCAGAGGGCAATGTTTCATAGTTTTTACT	2802	
1960	Qy	GCAATTCGATATCG	AGCTATG	GGCCATCG	GAAAAACGCTCGTTTGGCTCCCTGAATATCC	2019	
2803	Db	GCAATTCGATATCG	AGCTATG	GGCCATCG	GAAAAACGCTCGTTTGGCTCCCTGAATATCC	2862	
2020	Qy	AAAGCCAAATTC	GGGGGCTGG	CGCATCTGTTT	TGGCCCTGTTTGGAAAAAGAAACCAATATAGAC	2079	
2863	Db	AAAGCCAAATTC	GGGGGCTGG	CGCATCTGTTT	TGGCCCTGTTTGGAAAAAGAAACCAATATAGAC	2922	
2080	Qy	AGCGCAGTCA	AGAAAGGAAAAAGCC	CAGACACATG	TGAGGGAAATTTAGAGTTTCGAGAA	2139	
2923	Db	AGCGCAGTCA	AGAAAGGAAAAAGCC	CAGACACATG	TGAGGGAAATTTAGAGTTTCGAGAA	2982	
2140	Qy	GTCTCTTTCTTCTAT	CCATGTC	CGCCAGATGTTTT	CATCCTCGCTGGCTTATCCCTCAGT	2199	
2983	Db	GTCTCTTTCTTCTAT	CCATGTC	CGCCAGATGTTTT	CATCCTCGCTGGCTTATCCCTCAGT	3042	
2200	Qy	ATTGAGGGAGAA	AGACAGTAGCATTT	TGTTGGGAGCAG	CGGCTGTGGGAAAAAGCACTTCT	2259	
3043	Db	ATTGAGGGAGAA	AGACAGTAGCATTT	TGTTGGGAGCAG	CGGCTGTGGGAAAAAGCACTTCT	3102	
2260	Qy	GTTCAACTCT	CTGCAGAGACTT	TATGAC	CCCCGTGCAAGGACAAGTGCTGTTTGATGGTG	2319	
3103	Db	GTTCAACTCT	CTGCAGAGACTT	TATGAC	CCCCGTGCAAGGACAAGTGCTGTTTGATGGTG	3162	
2320	Qy	GATGCAAAAGAT	TGAATGTAC	AGTGGCTCCGTT	CCCAATAGCAATCGTTCTCTCAAGAG	2379	
3163	Db	GATGCAAAAGAT	TGAATGTAC	AGTGGCTCCGTT	CCCAATAGCAATCGTTCTCTCAAGAG	3222	
2380	Qy	CCGTGCTCTT	CAACTG	CAGCATTTG	TGAGACATCGCTATGCTGACACACCGCGTG	2439	
3223	Db	CCGTGCTCTT	CAACTG	CAGCATTTG	TGAGACATCGCTATGCTGACACACCGCGTG	3282	
2440	Qy	GTGCCATTTAG	TAGAGATCA	AAAGAGCCG	CAAAATGCGACAAATATCCATTCTTTTATTTGAA	2499	
3283	Db	GTGCCATTTAG	TAGAGATCA	AAAGAGCCG	CAAAATGCGACAAATATCCATTCTTTTATTTGAA	3342	
2500	Qy	GGTCTCCCT	GAGAAATAC	ACACAGATTT	GGACTGAAAGGACACAGCTTCTCTGGCGGC	2559	
3343	Db	GGTCTCCCT	GAGAAATAC	ACACAGATTT	GGACTGAAAGGACACAGCTTCTCTGGCGGC	3402	
2560	Qy	CAGAAA	CAAGA	CTAGCTATT	GCAAGGGCTCTTCTCCAAAAACCCAAAAATTTTATTTGTTG	2619	
3403	Db	CAGAAA	CAAGA	CTAGCTATT	GCAAGGGCTCTTCTCCAAAAACCCAAAAATTTTATTTGTTG	3462	
2620	Qy	GATGAGGCCA	CTTTCAG	CCCTCGATAT	ATGACAGTGGAGAGGTGTTT	CAGCTGCCCTTGAT	2679

Db 3463 GATGAGCCACTTCAGCCCTCGATAATACAGTGAAGGTGGTTTCAGCATGCCCTTGAT 3522
Qy 2680 AAAGCCAGGACGGGAAGCAGATGCTAGTGTCTCACTCAGAGGCTCTCTGCAATTCAGAAC 2739
Db 3523 AAAGCCAGGACGGGAAGCAGATGCTAGTGTCTCACTCAGAGGCTCTCTGCAATTCAGAAC 3582
Qy 2740 GCAGATTGATAGTGGTCTTCGCAANTGGAAGATAAAGAAACAAAGAACTCATCAAGAG 2799
Db 3583 GCAGATTGATAGTGGTCTTCGCAANTGGAAGATAAAGAAACAAAGAACTCATCAAGAG 3642
Qy 2800 CTCTGAGGAATCGAGACATATATTTAACTAGTGAATCCACAGTCAGTGCAGTGA 2856
Db 3643 CTCTGAGGAATCGAGACATATATTTAACTAGTGAATCCACAGTCAGTGCAGTGA 3699

RESULT 6
US-09-873-409-9
; Sequence 9, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Sayegh, Mohamed
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-9

Query Match 72.3%; Score 2066; DB 9; Length 2066;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 791 CGACAAAGTCGAGCTACATCTGTGTAGCACACGACCTTCTACTATTTCGAGTGCAG 850
Db 1 CGACAAAGTCGAGCTACATCTGTGTAGCACACGACCTTCTACTATTTCGAGTGCAG 60
Qy 851 ATTTGATTGACCTAAAGATGGAATGCTGGCGGAGAAAGAGACACATGCTCAACTAA 910
Db 61 ATTTGATTGACCTAAAGATGGAATGCTGGCGGAGAAAGAGACACATGCTCAACTAA 120
Qy 911 TGGCAAAACGAGGTCTATATTTACTTGTGTGATGTCACAGGATATTTAAAGAGCTGATG 970
Db 121 TGGCAAAACGAGGTCTATATTTACTTGTGTGATGTCACAGGATATTTAAAGAGCTGATG 180
Qy 971 AACAGTGGAGTCAATGACATATTTCTACTGAAGAAAGACCACTCACTTCTCTGCACT 1030
Db 181 AACAGTGGAGTCAATGACATATTTCTACTGAAGAAAGACCACTCACTTCTCTGCACT 240
Qy 1031 CTGTGAAGAGCATCAAGTCAGACTTCATTTGCAAGGCTGAGGAATCCACCAATCTTAAG 1090
Db 241 CTGTGAAGAGCATCAAGTCAGACTTCATTTGCAAGGCTGAGGAATCCACCAATCTTAAG 300
Qy 1091 AGATAAGTCTCTGAGTCTCTCTATTAAGTTTAAAGTTAAACAGCCTGAATGGC 1150
Db 301 AGATAAGTCTCTGAGTCTCTCTATTAAGTTTAAAGTTAAACAGCCTGAATGGC 360
Qy 1151 CTTTTGTGGTCTGGGACATGCTTCTGTCTTAAATGAACTGTTCATCCAGTATTTT 1210
Db 361 CTTTTGTGGTCTGGGACATGCTTCTGTCTTAAATGAACTGTTCATCCAGTATTTT 420
Qy 1211 CCATCATCTTGGAAAATTAACAGTGTGGAATTAATGATAAACCACATTAAGC 1270
Db 421 CCATCATCTTGGAAAATTAACAGTGTGGAATTAATGATAAACCACATTAAGC 480
Qy 1271 ATGATGAGAAATTTATTCAGTATATTCGTCATTTTGGGTGTTATTTGCTTCTCAGTT 1330

Db 481 ATGATGACAGAAATTTATTTCCATGATATTCGTCATTTTGGGTGTTATTTGCTTTGTGAGTT 540
Qy 1331 ATTTTCATGACGGATTTATTTTACGGCAGAGCAGGGGAAATTTTAAACGATCAGATTAAAGAC 1390
Db 541 ATTTTCATGACGGATTTATTTTACGGCAGAGCAGGGGAAATTTTAAACGATCAGATTAAAGAC 600
Qy 1391 ACTTGGCCCTTCAAGCCATGTTATATCAGGATATTTGCTGCTGGTTTGTATGAAGAGAAACA 1450
Db 601 ACTTGGCCCTTCAAGCCATGTTATATCAGGATATTTGCTGCTGGTTTGTATGAAGAGAAACA 660
Qy 1451 GCACAGGAGCTTGCACAAATATTAGCCATAGATATAGACAAATTTCAAGGAGCAACAG 1510
Db 661 GCACAGGAGCTTGCACAAATATTAGCCATAGATATAGACAAATTTCAAGGAGCAACAG 720
Qy 1511 GTTCCAGGATTCGCTTTTAAACAAATATGCAATTAACATGAGGACCTTTTCACTTATCATTT 1570
Db 721 GTTCCAGGATTCGCTTTTAAACAAATATGCAATTAACATGAGGACCTTTTCACTTATCATTT 780
Qy 1571 CTTTATATATGATGGGAGATGACATTCCTGATTCGAGTATTTGCTCCAGTACTTTGCCG 1630
Db 781 CTTTATATATGATGGGAGATGACATTCCTGATTCGAGTATTTGCTCCAGTACTTTGCCG 840
Qy 1631 TGACAGGAATGATTTGAAACCCGACGCAATGACTTGGATTTCCCAACAAAGATAAGCAAGAAC 1690
Db 841 TGACAGGAATGATTTGAAACCCGACGCAATGACTTGGATTTCCCAACAAAGATAAGCAAGAAC 900
Qy 1691 TTAAGCATCTCGAAGATAGCAATCGAGCTTTGAGGATATACGTACTATAGTCTCAT 1750
Db 901 TTAAGCATCTCGAAGATAGCAATCGAGCTTTGAGGATATACGTACTATAGTCTCAT 960
Qy 1751 TTAACAGCAAAAGAGCTTCGAGCAAAATGATGAAGAGATGCTTTCAGACTCAACACAGAA 1810
Db 961 TTAACAGCAAAAGAGCTTCGAGCAAAATGATGAAGAGATGCTTTCAGACTCAACACAGAA 1020
Qy 1811 ATACCTCGAAGAAAGCACAGATATTTGGAAGCTTTTATGCAATTCAGCCATGCTTTATAT 1870
Db 1021 ATACCTCGAAGAAAGCACAGATATTTGGAAGCTTTTATGCAATTCAGCCATGCTTTATAT 1080
Qy 1871 ATTTTCCCTATGACAGAGGCTTTCGATTTGGAGCCTTATTAATTCAGCTGGAAGCAATGA 1930
Db 1081 ATTTTCCCTATGACAGAGGCTTTCGATTTGGAGCCTTATTAATTCAGCTGGAAGCAATGA 1140
Qy 1931 CCCAGAGGCAATGTTTCATAGTTTTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA 1990
Db 1141 CCCAGAGGCAATGTTTCATAGTTTTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA 1200
Qy 1991 AAACGCTCGTTTGGCTCTGAAATATTCGAAAGCCTTTCGAAAGCCTTTCGAAAGCCTTTCGAA 2050
Db 1201 AAACGCTCGTTTGGCTCTGAAATATTCGAAAGCCTTTCGAAAGCCTTTCGAAAGCCTTTCGAA 1260
Qy 2051 CTTTGTGGAAAGAAACCAATATAGACAGCCGCAATTCAGAGGAGGAAAGGAAAGGAAAGGAAAG 2110
Db 1261 CTTTGTGGAAAGAAACCAATATAGACAGCCGCAATTCAGAGGAGGAAAGGAAAGGAAAGGAAAG 1320
Qy 2111 CATGTGAAGGATTTAGAGTTTCGAGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2170
Db 1321 CATGTGAAGGATTTAGAGTTTCGAGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
Qy 2171 TTTTTCATCTCTCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAAGACAGTAGCATTTTGTGG 2230
Db 1381 TTTTTCATCTCTCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAAGACAGTAGCATTTTGTGG 1440
Qy 2231 GGAGCAGCGCTGTGGGAAAGACATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2290
Db 1441 GGAGCAGCGCTGTGGGAAAGACATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
Qy 2291 TGCAGACCAAGTGTCTTGTGATGTTGATGTCGAAAGAAATGAAATGTAAGTGTACAGTGGCTCC 2350
Db 1501 TGCAGACCAAGTGTCTTGTGATGTTGATGTCGAAAGAAATGAAATGTAAGTGTACAGTGGCTCC 1560
Qy 2351 GTTCCCAAAATAGCAATGTTTCTTCAAGAGCTGTGCTTCTTCAACGTGAGCATTTGCTGAGA 2410
Db 1561 GTTCCCAAAATAGCAATGTTTCTTCAAGAGCTGTGCTTCTTCAACGTGAGCATTTGCTGAGA 1620

2411 ACATCGCCTATGGTGACACAGCGGTGGTGCATTAGATGAGATCAAGAGCGCGAA 2470
Db ACATCGCCTATGGTGACACAGCGGTGGTGCATTAGATGAGATCAAGAGCGCGAA 1680
Qy ATGAGCAAAATATCCATCTTTATTGAAGGTCTCCCTGAGAAATACACACAAGTTG 2530
Db ATGAGCAAAATATCCATCTTTATTGAAGGTCTCCCTGAGAAATACACACAAGTTG 1740
Qy GACTGAAAGGAGCAGCAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGCTC 2590
Db GACTGAAAGGAGCAGCAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGCTC 1800
Qy TTCTCCAAAAACCCAAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATTAATGACA 2650
Db TTCTCCAAAAACCCAAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATTAATGACA 1860
Qy GTGAGAGGTGTTTTCAGCATGCGCTTTGATAAGCCAGGAGCGGAGGACATGCTAGTGG 2710
Db GTGAGAGGTGTTTTCAGCATGCGCTTTGATAAGCCAGGAGCGGAGGACATGCTAGTGG 1920
Qy TCACATCAGAGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGTCTGACAAATGAA 2770
Db TCACATCAGAGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGTCTGACAAATGAA 1980
Qy AGATAAGGACAGAGGACTATGAGAGCTCTGAGAAATCGAGACATATTTTAAGT 2830
Db AGATAAGGACAGAGGACTATGAGAGCTCTGAGAAATCGAGACATATTTTAAGT 2040
Qy TAGTGAATGACAGTCAGTCAGTCAGTCA 2856
Db TAGTGAATGACAGTCAGTCAGTCAGTCA 2066

RESULT 7
US-10-092-900A-303
; Sequence 303, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Kieper, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A

CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 303
; LENGTH: 4091
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(4078)
US-10-092-900A-303

Query Match 58.0%; Score 1657.2; DB 13; Length 4091;
Best Local Similarity 78.0%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 508; Indels 117; Gaps 14;
Qy 115 TTTTCTTTAGTGAATCCATAGCAGTTATGCAATGAGAGCAGTCCCTCATTTATGAT 174
Db 1072 TTGCTCTCTGATATTCCTCAAGGCAATCGGGGGCTGCGCATCTGTTGCTTTGGAA 1131
Qy 175 AAGAAACCCAGTATAGATTAATTTCCACAGCTGATATAAAC-----TGAATCCATA 228
Db 1132 AAGAAACCAATATAGACGCCAGCTCAGAGGGAAGAAAGCAGTAGACGACATGT 1191
Qy 229 GAAGGAACCTCGGAATTTAAATAATGTTTCTTCAATATCCATCAAGACCATCTATCAAG 288
Db 1192 GAAGGAATTTAGAGTTTCGAGAAAGTCTCTTCTCTATCCATGTCGCCAGATGTTTC 1251
Qy 289 ATTCTGAAGGTCTGAATCTCAGATTAAGTCTGGAGAGACACTGCGCTTGGTGGTCTC 348
Db 1252 ATCTTCGCTGGCTTATCCCTCAGTATGAGCGAGGAAGACAGTAGCATTTGTGGGAGC 1311
Qy 349 AATGGCAGTGGGAGAGTAGTACGGTAGTCCAGCTTCTGACAGGTTATATGATCCGATGAT 408
Db 1312 AGCGGCTGTGGAAAGACACTTCTGTTCAACTTCTGACAGAGACTTTATGACCCCGTCAA 1371
Qy 409 GGCTTTATCATGTGTGATGAGATGACATCAGAGCTTTAAATGTCGGCATTATCGAGAC 468
Db 1372 GG-----ACAAGTGGATGGTGTGGATGCAAAAGAAATTGAATGTACAGTGGCTCCGTTCC 1425
Qy 469 CATATTGGAGTGGTTAGTCAAGAGCCCTGTTTCTGGGACCCACCACCATCAGTAACATATC 528
Db 1426 CAATAGCAATCGTTCTCAAGAGCCCTGCTCTTCACTGACAGCAATTGCTGAGAACATC 1485
Qy 529 AAGTATGG-----ACGAGATGATGCTGATGAAGAGATGGAGAGAGCAGCAGAGGAA 582
Db 1486 GCCTATGTTGACACACAGCCCGTGTGGTGGCCATTAGATGAGATCAAGAGAGCGCAATGCA 1545
Qy 583 GCAATGCGTATGATTTTATCATGAGTTTCTTAATAAATTTAATACATTTAGTAGGGGAA 642
Db 1546 GCAATATCCATTTCTTTTATGAGGTTCTCCCTGAGAAATACACACACAGTTGGACTG 1605
Qy 643 AAAGGAGCTCAATGAGTGGAGGGGAGAAACAGAGGATCGCAATTTGCTGCTTAGTT 702

2686	Db	GCAATGACTGGATTTTCCCAACAAGATAAGCAAGAACTTAAGCATGCTGGAAAGGTTAAG	2745
1708	Qy	ATAGCAACTGAAGCTTTGGAGAAATATACGTACTATATAGTGTCAATTAAACAAGGGAAGAAAGCC	1767
2746	Db	ATAGCAACTGAAGCTTTGGAGAAATATACGTACTATATAGTGTCAATTAAACAAGGGAAGAAAGCC	2805
1768	Qy	TTGAGCAAAATGTATGAGAGATGCTTCAGACTCAACAC---AGAAATACCTCGAAGAA	1824
2806	Db	TTGAGCAAAATGTATGAGAGATGCTTCAGACTCAACACAGGAGAAATACCTCGAAGAA	2865
1825	Qy	GCACAGATTATTGGAAGCTGTATGCATTCAGGCATGCCCTTTATATATATTTCCTATGCA	1884
2866	Db	GCACAGATTATTGGAAGCTGTATGCATTCAGGCATGCCCTTTATATATATTTCCTATGCG	2925
1885	Qy	GCAGGGTTTCGATTTGGAGCCTATTAAATTCAGCTGGAGCAATGACCCAGAGGGCGATG	1944
2926	Db	GCAGGGTTTCGATTTGGAGCCTATTAAATTCAGCTGGAGCAATGACCCAGAGGGTTTATCT	2985
1945	Qy	TT---CATAGTTTTTATCGAAATTCGATATGGAGCTATGCCATCGGAAAGAAACGCTCGTT	2001
2986	Db	TTTGATAGAGTTTTTACTGCAAATTCGATATGGAGCTATGGCCATCGAGAAACGCTCGTT	3045
2002	Qy	TTGCTCTCTGAATATTCCAAAGCCAAATCGGGGGCTGCGCATCTGTTTGCCTTGTGGAA	2061
3046	Db	TTGCTCTCTGAATATTCCAAAGCCAAATCGGGGGCTGCGCATCTGTTTGCCTTGTGGAA	3105
2062	Qy	ARGAAACCAATATAGACAGCCGCTCAAGAGGGGAAAGGCA-----GACACA	2112
3106	Db	ARGAAACCAATATAGACAGCCGCTCAAGAGGGGAAAGGCACTTTCACAGGACACA	3155
2113	Qy	TGTGAAGGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTTATCCATGTCGCCCAGATGTT	2172
3166	Db	TGTGAAGGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTTATCCATGTCGCCCAGATGTT	3225
2173	Qy	TTCAATCTCCGTGGCTTATCCCTCAGTATTGACGAGGAAAGACAGTAGCATTTGTGGG	2232
3226	Db	TTCAATCTCCGTGGCTTATCCCTCAGTATTGACGAGGAAAGACAGTAGCATTTGTGGG	3285
2233	Qy	AGCAGGGCTGTGGGAAAGCACTTCGTTCAACTTCTGCAGAGACTTTATGACCCCGTG	2292
3286	Db	AGCAGGGCTGTGGGAAAGCACTTCGTTCAACTTCTGCAGAGACTTTATGACCCCGTG	3345
2293	Qy	CAGGACAAAGTCTGTGTTGATGTGGATGCAAAAGAAATGAAATGATCAGTGGCTCCGT	2352
3346	Db	CAGGACAAAGTCTGTGTTGATGTGGATGCAAAAGAAATGAAATGATCAGTGGCTCCGT	3405
2353	Qy	TCCCAATAGCAATCGTTCCCTCAAGAGCTGTGCTCTTCAACTGACAGCTTGTGTGAGAAC	2412
3406	Db	TCCCAATAGCAATCGTTCCCTCAAGAGCTGTGCTCTTCAACTGACAGCTTGTGTGAGAAC	3465
2413	Qy	ATCGCTATGGTGACCAACAGCCGTGTGTGGCCATTAGATGAGATCAAGAGCGCGCAAT	2472
3466	Db	ATCGCTATGGTGACCAACAGCCGTGTGTGGCCATTAGATGAGATCAAGAGCGCGCAAT	3525
2473	Qy	GCAGCAAAATCCATCTTTTATTGAGGTCTCCCTGAGAAATACACACACAAGTTTGA	2532
3526	Db	GCAGCAAAATCCATCTTTTATTGAGGTCTCCCT---AAATACACACAAGTTTGA	3582
2533	Qy	CTGAAAGGAGCAGAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTT	2592
3583	Db	CTGAAAGGAGCAGAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTT	3642
2593	Qy	CTCCAAAACCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATATGACAGT	2652
3643	Db	CTCCAAAACCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATATGACAGT	3702
2653	Qy	GAGA-----AGGTGGTTTCAGCATGCCCCTTGATAAAGCCAGGACGGGAAGCATGCTTA	2706
3703	Db	GAGAAGGTACAGGTGGTTTCAGCATGCCCCTTGATAAAGCCAGGACGGGAAGCATGCTTA	3762
2707	Qy	GTGGTCACTCAGAGGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGGTTCTGCACAAT	2766
3763	Db	GTGGTCACTCAGAGGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGGTTCTGCACAAT	3822

QY 2767 GGAAAGATAAAGGAAACAGGAACTCATCAAGAGCTCTGAGAAATCGAGACATATATTTT 2826
Db 3823 GGAAAGATAAAGGAAACAGGAACTCATCAAGAGCTCTGAGAAATCGAGACATATATTTT 3882
QY 2827 AAGTTAGTGAATGCACAGTCAGTG 2850
Db 3883 AAGTTAGTGAATGCACAGTCAGTG 3906

RESULT 8

US-09-805-020-30
; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30

Query Match 36.1%; Score 1030.2; DB 13; Length 4533;
Best Local Similarity 62.2%; Pred No. 4e-269;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
QY 166 ATATTGATAAGAAACCCAGTATAGATAAATTTTCCACAGCTGGATATAAACCCTGAATCC 225
Db 1526 ATAATTGATAAAGCCAAAGTATTGACAGCTATTCCGAAGAGTGGGCACAAACCAGATAAT 1585
QY 226 ATAGAGGAACTGCGAATTTAAATATTTCTTTCAATATCCATCAAGACCCTATC 285
Db 1586 ATTAGGAAATTTGGAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAGAGTT 1645
QY 286 AAGATTCTGAAGGCTGTAATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTGGTGGT 345
Db 1646 AAGATCTTGAAGGCTGTAATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTGGTGGT 1705
QY 346 CTCATGTCAGTGGGAGAGTACGCTAGTCCAGCTTCTCGAGAGCTTATATGATCCGAT 405
Db 1706 AACAGTGGCTGGGAGAGACAAACAGCTCCAGCTGATGAGAGGCTCTATGACCCACA 1765
QY 406 GATGGCTTTATCATGTGGATGAGAAATGACATCAGAGCTTTAAATGTGCGGCATTAATCGA 465
Db 1766 GAGGGATGTCAGTGTTCATGAGACAGGATAATTAGACCATAAATGTAAGGTTTCTACGG 1825
QY 466 GACCATATGAGTGGTGTAGTCAAGAGCTGTTTGTTCGGACACCATCATGTAACAT 525
Db 1826 GAAATCATTTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1885
QY 526 ATCAAGTATGAGACAGATGATGCTGATGAAGAGATGGAGAGAGCAGCAGGAGGAGCA 585
Db 1886 ATTCGATATGGCTGAAATGTCACCATGATGAGATGAGAAAGCTGTCAGGAGGCC 1945
QY 586 AATGCTATGATTTATCATGAGGTTTCTTAATAATTTTAATATATTTGTTAGGAGGAGAAA 645
Db 1946 AATGCTATGATTTATCATGAACTGCTCTATAAATTTGACACCCCTGGTTGAGAGAGA 2005
QY 646 GGAGCTCAATAGTGGAGGAGAAACAGAGATCGCAATTTGCTGTCCTTTAGTTGCA 705
Db 2006 GGGGCCAGTTGAGTGGTGGGAGAGAGAGATCGCATTTGACATTTGACCTTGGTTGCG 2065
QY 706 AACCCCAAGATTCTGATTTTAGATGAGGCTAGCTGTGCTGCCCTGGATTCAGAAAGCAAGTCA 765

Db 2066 AACCCCAAGATTCTGCTGCTGATGAGGCCAGCTCAGCCTTGGACACAGAAACGAGCA 2125
QY 766 GCTGTTCAAGCTGCTCACTGGAGAGGCGAGCAAGAGTTCGGAATCTGATGAGCAGC 825
Db 2126 GTGGTTCAAGCTGCTCACTGGAGAGGCGAGCAAGAGTTCGGAATCTGATGAGCAGC 2185
QY 826 CGACTTTTCACTATTCAGAGTGCAGATTTGATGTCACCTAAAGAGTGCAGTGGCG 885
Db 2186 CGTTTGTCTACAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2245
QY 886 GAGAAAGGAGCAGATGCTGAACTAATGCGAAACAGAGGCTCTATATTTATTCATCTTGTGATG 945
Db 2246 GAGAAAGGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2305
QY 946 TCACAGGATATTAAGAGCTGATGAACAGATGAGAGTCAATGATCAATTTCTA----- 997
Db 2306 ATGCAGACAGCAGGAAATGAAGTTGAATTTAGAAATTCGAGCTGATGAATTCAGAAAGTAA 2365
QY 998 -----CTGAAAGAAACAGCAACTCACTTCTCTGCACTCTGCAAGAGCATCA--- 1045
Db 2366 ATTGATGCTTGGAAATGCTTCAATGATTCAGATTCAGTCTTAATAGAAAAGATCA 2425
QY 1046 -----AGTCAGACTTCATTTGAAGGCTGAGGATCCAGCAATCCAGCAATCT 1086
Db 2426 ACTCGTAGGAGTGTCCGTGATCAAGGCCAAGACAGAGAGCTTAGTACCAAGAGGCT 2485
QY 1087 AAGAGATAGTCTTCTGAGTCTCTATTAATAAATTTTAAAGTTTAAACAGAGCTGAA 1146
Db 2486 CTGATGAAGATATCTCTCAAGTTTCTTTTGGAGATATGAGCTTAATTTAACTGAA 2545
QY 1147 TGCCCTTTTGTCTTGGGACATTTGGCTTCTTCTAAATGGAACATGTTTCAATCCAGTA 1206
Db 2546 TGCCCTTTTGTCTTGGGATTTTGTGCTTATTTTGTGCTTATTAATTAAGAGCTTCAACAGCA 2605
QY 1207 TTTTCCATCATCTTCCAAATAATTAACCATGTTTGGAAATTAATGATTAACACACATTA 1266
Db 2606 TTTTCCATTAATTTTCAAGATATTAAGGCTTTTCAAGAAATTTGATGATCTCTGAAACA 2665
QY 1267 AAG---CATGATGAGAAATTTTATTCATGATATTCGTCTATTTTGGGTGTTTATTTGCTTT 1323
Db 2666 AAGCAGAGAAATAGAACTTTTTCATTTTCTAGCCCTTGGAAATTTATTTCTTTT 2725
QY 1324 GTGATTTATTCAGAGGATTTTTCAGCAGAGCAGGAGGAAATTTTAAAGATGAGA 1383
Db 2726 ATTACATTTTCTTCCAGGCTTTTCAATTTGGCAAGCTGAGAGATCTTCAACAGCGG 2785
QY 1384 TTAAGACATTTGGCTTCAAGGCTATGTTATATCAGGATTTGCTGCTGTTTGTATGAAG 1443
Db 2786 CTCGATACATGTTTTCGATCCATGCTCAGACAGGATGAGTTGTTTGTATGACCT 2845
QY 1444 GAAACAGCAGAGGCTTGAACAAATTTAGCCATAGATATAGCAGAAATTCAGGA 1503
Db 2846 AAAAAACACCACTGGAGCAATGACTACCAAGCTCGCCAAATGATGCTGCTCAAGTTAAAGGG 2905
QY 1504 GCAACAGTTTCCAGATTTGGCTTAAACACAAATGCAATTAACATGGGACTTTTCAGTT 1563
Db 2906 GCTATAGTTTCCAGGCTTGTGTAATTTACCAGATATAGCAATCTTGGGACAGGAATA 2965
QY 1564 ATCATTTCTTTATATGATGAGAGATGACATTCCTGATTTCTGATTTTGTCTTCCAGTA 1623
Db 2966 ATTATATCTTCTATGTTTGGCACTAACACTGTTACTCTTTAGCAATTTGTACCCATC 3025
QY 1624 CTTCCTGTCAGAGAAATGATTGAAACCGCAGCAATGATGATTTGCAACAAAGATAAG 1683
Db 3026 ATTGCAATAGCAGAGTTGTTGAATGAATGTTGTTGTCGACAGCACTCAAGAGATAAG 3085
QY 1684 CAAGAATCTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGATATATACGTACTATA 1743
Db 3086 AAAGAATCTAGAAGGCTGCGGAGAGATCGCTACTGAAGCAATAGAAATCTTCGAAACGCTT 3145
QY 1744 GTGTCATTACAAAGGAAAGCCCTCGAGCAATGATGATGAAGAGATGCTTCAGACTCAA 1803

Db 3146 GTTCTTTTGACTCAGGAGCAGAGTTTGAACATATGTATGCTCAGAGTTTGCAGGTACCA 3205
Qy 1804 CACAGAAATACCTTCGAGAGACACAGATTATTGGAGCTGTATTGATTCAGCCATGCC 1863
Db 3206 TACAGAAATCTTTTGAGAAAGACACATCTTTTGGATTAATATTTCTTCCACCCAGGA 3265
Qy 1864 TTTATATATTTTCCATGATCAGAGGGTTTCGATTTTGGAGCTTATTAATTTCAAGCTGA 1923
Db 3266 ATGATGTAATTTTCTTATGCTGAGATGTTCCGGTTTGGAGCTTACTTGTGTGCACATAA 3325
Qy 1924 CGATGACCCACAGAGCAATTTCAATGTTTCTACGCAATTCATATGAGCTATGGCTGGCC 1983
Db 3326 CTATGAGCTTTGAGGATGTTCTTGTAGTATTTTTCAGCTGTGTCTTGTGTGCATGGCC 3385
Qy 1984 ATCGGAAAAACGCTGCTTTTGGCTCCTGAAATATTTCCAAAGCCAAATCGGGGGCTGGCAT 2043
Db 3386 GTGGGCACTGATGTTCAATTTGCTCCTGACTATGCCAAGCCAAATATCAGCAGCCAC 3445
Qy 2044 CTGTTGCTCTGTTGGAAGAAACCAATATAGACAGCGGAGTCAAGAGGAAAG 2103
Db 3446 ATCATCATGATCATTTGAAAGAAACCCCTTTGATGACAGCTACAGCAGCGGAAGCCCTAATG 3505
Qy 2104 CCAGACATGTGCAAGGAAATTAGAGTTTCGAGAGTCTCTTTCTTCTATCCATGCTGC 2163
Db 3506 CCGAACACATTTGAGGAATGTCACATTTGGTGAAGTTGTATTCACTATCCACCCGA 3565
Qy 2164 CCAGATGTTTTCATCTCTGCTGCTTATCCCTCAGTATTGAGCGAGGAAGACAGTAGCA 2223
Db 3566 CCGCAATCTCCAGTCTTTCAGGACTCAGCTCGAGGTGAAGAGGCGCAGACCTGGCT 3625
Qy 2224 TTTGTGGGAGCAGCGCTGTGGGAAGACACTCTGTTTCAACTCTCTGCAGAGACTTTAT 2283
Db 3626 CTGGTGGAGCAGTGTGCTGTGGAGAGACAGTGTCTGCTCTCTGAGCGGTTCTAC 3685
Qy 2284 GACCCCTGCAAGGACAAAGTCTGTTTGTGATGTTGAGTGCAGAAAGAAATTTGAATGTAAG 2343
Db 3686 GACCCCTTGGCAGGAAAGTCTGTTGATGGCAAGAAATTAAGCGACTGAATGTTTCAAG 3745
Qy 2344 TGGCTCGTTCCAAATAGCAATCTGTTCTCAGAGCTGTGCTCTTCACTGACAGATT 2403
Db 3746 TGGCTCGAGCACCTCGGCACTCGTGTCCAGAGCCCATCTGTTTGTACTGACAGATT 3805
Qy 2404 GCTGAGAAATCCCTATGTGACACAGCGCTGTGTGTCATTAGATGAGATCAAGAA 2463
Db 3806 GCTGAGAACATCTGCTATGAGACACAGCGGGTGTGTCAAGAGAGATCGTAGG 3865
Qy 2464 GCGGAAATGCGAAATATTCATTTCTTTTATTTGAAGTCTTCCCTGAGAAATACACACA 2523
Db 3866 GCAGCAAGGAGGCGCAACATACATGCTTCAATGAGTCACTGCTTAATAATATAGCACT 3925
Qy 2524 CAAAGTTGACTGAAAGAGCACAGCTTTCTGGGCGCAGAAACAAAGACTAGCTATTGCA 2583
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Qy 2584 AGGCTCTTCTCCAAAGCCCAAAATTTTATTTGATGAGGCGCACTTCAGCCCTCGAT 2643
Db 3986 CGTGCCTTTGTAGACGCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGAT 4045
Qy 2644 AATGACAGTGAAGTGTGTTGATGATGCTTGTATTAAGCCAGGAGGAGGAGCATGC 2703
Db 4046 ACAGAAAGTGAAGGTTGTTCCAGAGGCGCTGCAAGAGCCAGAGAGGCGCGCACTGC 4105
Qy 2704 CTAGTGTCTACCTCAGAGCTCTCTGCAATTCAGAAAGCAGATTTGATGAGTGTCTGCAC 2763
Db 4106 ATTGTGATGCTCAGCGCTGTCCACCATCCAGAAATGACAGCTTATAGTGTGTTTCAAG 4165
Qy 2764 AATGGAAGTAAAGGACAGAGAACTCATCAGAGCTCTGAGAAATCGAGACATATAT 2823
Db 4166 AATGGCAGAGTCAAGGAGCATGCAACGATCAGCAGCTGCTGGCAGAGAAAGGCATCTAT 4225
Qy 2824 TTTAAGTTAGTGAATGACAGTCAAG 2848
Db 4226 TTTTCAATGTCAGTGTCCAGGCTG 4250

RESULT 9

US-10-072-621-2
; Sequence 2, Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2

Query Match 36.1%; Score 1030.2; DB 14; Length 4643;
Best Local Similarity 62.2%; Pred. No. 4,1e-269; Indels 42; Gaps 3;
Matches 1695; Conservative 0; Mismatches 988;

Qy 166 ATTATGTATAAGAAACCCAGTATAGATAACTTTTCCAGCTGGATATAAAACCTGAATCC 225
Db 1523 ATAAATTTGATTAATAGCCCAAGTATTGACAGCTATTGGAAGAGTGGGCACAAACCGAGATAT 1582
Qy 226 ATAGAGGAACTGTGGAATTTAAATAATGTTCTTTCAATTTATCCATCAAGACCATCTATC 285
Db 1583 ATTAAGGGAATTTTGGAAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAGAAAGTT 1642
Qy 286 AAGATTCTGAAAGGTCTCGAATCTCGAATTAAGTCTGGAGAGACAGTCCGCTTGTCTGGT 345
Db 1643 AAGATCTTGAAGGGTCTCGAATCTGGAAGTGCAGAGTGGCGCAGACGGTGGCTGTTGGA 1702
Qy 346 CTCATGTCAGTGGGAAAGTACGGTACTGCTTCCAGCTTCTGCGAGAGTTATAGATCCGGAT 405
Db 1703 AACGTGGCTGTGGGAAGAGCACACAGTCCAGCTGATGTCAGAGGCTCTATGACCCACA 1762
Qy 406 GATGCTTTTATCATGCTGGATGAGAAATGACATCAGAGCTTTAAATGTGGCGCAATTATCGA 465
Db 1763 GAGGGATGGTCAGTGTGTGATGGACAGGATATTAGCACCAATAATGTAAGTTTCTACGG 1822
Qy 466 GACCAATTTGGAGTGTGTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAT 525
Db 1823 GAAATCATTTGGTGTGTGAGTCAAGAACTGTGTTTGTTCGCCACCAACGATAGCTGAAAC 1882
Qy 526 ATCAAGTATGGACGAGATGATGTGACTGATGAAGAGATGGAGAGAGCAGCAGCAAGCA 585
Db 1883 ATTCGCTATGGCCGTGAAAATGTCTCCATGGATGAGATTGAGAAAGCTGTCTAGAGAGCC 1942
Qy 586 AATGGTATGATTTTATCATGAGTTCCTTAATAAATTTAATACATTTGGTAGGGGAAAA 645
Db 1943 AATGCTATGACTTTTATCATGAATCTGCTCATAAATTTTGACACCTGTTGGAGAGAGA 2002
Qy 646 GGAGTCAATGAGTGGGAGGCGAGAAACAGAGGATCGCAATTTGCTGCTGCTTACTTGA 705
Db 2003 GGGGCCCAAGTTGAGTGGTGGGCGAAGCAGAGGATCGCCATTTGACAGCTGCTGTTTGC 2062
Qy 706 AACCCCAAGATTCTGATTTTATGATGAGGCTACGCTGCTGCCCTGGATTTCGAAAGCAAGTCA 765
Db 2063 AACCCCAAGATCTCTCTGCTGATGAGGCGACGTCAGCTTGGACACAGAAAGCGAAGCA 2122
Qy 766 GCTGTTCAAGTGCATCTGGAGAGCGGAGCAAGGTGCGACTCAATGTTGGTAGCACAC 825
Db 2123 GTGGTTCAGGTGCTCTGATTAAGGCCAGAAAGGTGCGACCAACCAATTTGTGATAGCTCAT 2182
Qy 826 CGACTTTCTACTATTTCGAAAGTGCAGATTTGATTTGAGCCCTAAAGAGATGGAATGCTGGC 885

Db 2183 CGTTGCTCAGATTCGTGTAAGTCTGACGCTCATCGCTGCTTTCGATGATGGAGTCAATTGTG 2242
Qy 886 GAGAAAGGACACATGCTGAACTAATGCAAAACGAGGTCTATATTAATTCATCTGTGATG 945
Db 2243 GAGAAAGGAAATCATGATGAATCATGAAAGAGAAAGGCAATTAATCTCAAACTGTGACA 2302
Qy 946 TCACAGGATATTAAGAGCTGATGAACAGATGAGTCAATGACATATCTA----- 997
Db 2303 ATGCACAGCAGAGAAATGAAGTTGAATAGAAATGCGCTGATGAATCCAAAGTGAA 2362
Qy 998 -----CTGAAGAAAGACCAACTCACTTCCTCTGCACTCTGTGAGAGCATCA--- 1045
Db 2363 ATTGATGCTTGGAAATGCTTCAATGANTCAAGATCCAGTCTAATAAGAAAGATCA 2422
Qy 1046 -----AGTCAGACTTCATTGACAGGCTGAGGAATCCACCAATCT 1086
Db 2423 ACTGCTAGAGTGCTCGGTGATCAAGCCCAAGCAGAGAAAGCTTAGTACCAAGAGGCT 2482
Qy 1087 AAAGAGATAAGTCTTCCTGAAAGTCTCTATTAATAAAATTTTAAAGTTTAAACAGGCTGAA 1146
Db 2483 CTGGATGAAGATATACCTCCAGTTCTCTTTTGGAGGATTAAGAGCTAAATTTAACTGAA 2542
Qy 1147 TGGCCTTTTGTGTTCTGGGACATTTGGCTTCTGTTCTAAATGGAATGTTTCATCCAGTA 1206
Db 2543 TGGCCTTATTTGTTGTTGTTGTTTGTGCTCATTTAATATGAGGCTTGAACCCAGCA 2602
Qy 1207 TTTTCCATCATCTTTGCAAAATATACCATGTTTGGAAATATGATAAACACATTA 1266
Db 2603 TTTGCAATATATTTTCAAGATATAGGGTTTATACAGAAATGATGATCCTGGAACA 2662
Qy 1267 AAG----CATGATGCAAGAAATTTATCCATGATTTCTGTCATTTGGGTTTATTTGCTTT 1323
Db 2663 AAACGACAGAAATAGTAACTGTTGTTTCACTATTTGTTTCTAGCCCTTGGAAATATTTCTTTT 2722
Qy 1324 GTGATTTATTCATGACGGGATTTATTTACGCGAGAGCAGGAGAAATTTTAAACATGAGA 1383
Db 2723 ATTACATTTTCTTACGGTTTACATTTGCAAGCTTGAGAGATCCTCACAGGG 2782
Qy 1384 TTAGACACTTGGCCTTCAAGCCATGTTATATCAGGATATTTGCTGTTTATGATGAAG 1443
Db 2783 CTCCTGATACATGTTTCCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGTATGACCT 2842
Qy 1444 GAAACACGACAGAGGCTTGCAACATATATAGCATAGATATAGCAAAATTTCAAGGA 1503
Db 2843 AAAAACACCTGGAGCATGACTACACAGGCTCGCCATGATGCTGCTCAAGTTTAAAGG 2902
Qy 1504 GCAACAGGTTCCAGATTTGGGCTTTTAAACAAATGCAATTAACATGGGACTTTCAGTT 1563
Db 2903 GCTATAGTTTCCAGGCTTGTATATACCAGAAATATAGCAATCTTTGGCACAGGAATA 2962
Qy 1564 ATCATTTCTTTATATGATGGATGGAGATGACATTCGTATCTGATTTGCTCCAGTA 1623
Db 2963 ATTATATCTTCACTATGTTGGCACTAAACACTGTTACTCTTAGCAATTTTACCCATC 3022
Qy 1624 CTTGCGCTGACAGGAATGATGAACCCGACGCAATGACTGGATTTGCCAAACAAAGATAAG 1683
Db 3023 ATTGCAATAGCAGGAGTTGTTGAATGAAATGTTGCTGCAAGCACTGAAAGATAG 3082
Qy 1684 CAAGAACTTAGCATGCTGGAAGATAGCAACTGAGCTTTGGAGATATACGTACTATATA 1743
Db 3083 AAAGAACTAGAGGTTGCTGGAGATGCTCTACTGAAGCAATAGAAATCTCCGAACCGTT 3142
Qy 1744 GTGCTATTAAAGGGAAGGCTTTCAGAGCAATGATGAAGAGATGCTTCAGACTCAA 1803
Db 3143 GTTCTTTGACTCAGAGCAGAGATTTGAAATATGATGTTGCTCAGAGTTGCAAGTACCA 3202
Qy 1804 CACAGAAATACCTCGAAGAAAGCAGATTAATTTGAAGCTGTTATGCAATTCAGCCATGCC 1863
Db 3203 TACAGAACTCTTTGAGGAAAGCACAATCTTTTGAATTTACATTTTCTTCCACCCAGGCA 3262
Qy 1864 TTTATATATTTGCTCTATGACAGGCTTTTCGATTTGGAGCTATTTAATTTCAAGCTGGA 1923
Db 3263 ATGATGATTTTCTTATGCTGGATGTTTCCGTTTGGAGCTTACTTGGTGGCAATAA 3322

Qy 1924 CGAATGACCCCGAGAGGGCATGTTTATAGTTTATCTGCAATTTGCATATGAGAGCTATGGCC 1983
Db 3323 CTATGAGCTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTTGTTGTTGTTGCTATGGCC 3382
Qy 1984 ATCGGAAAAAGCTGCTTTTGGCTCTGTAATATTTCCAAAGCCAAATTCGGGGGCTGGCCAT 2043
Db 3383 GTGGGCGAGTCACTGTTCTGCTGACTATGCCAAGCCAAATATATCAGCAGCCAC 3442
Qy 2044 CTGTTTGGCTTTGTTGAAAAAGAAACCAATATATAGACGCGGAGTCAAGAGGGAAG 2103
Db 3443 ATCATCATGATCATTTGAAAAACCCCTTTGATGACAGCTACACGACGGAAGCCCTAATG 3502
Qy 2104 CCAGACACATGTCAGGGAATTTAGAGTTTTCAGAGAGTCTCTTTCTTCTATCATCTGCG 2163
Db 3503 CCAGACACATTTGAGAGGAATGTCAATTTGTTGAAATTTGATTTCACTATCCACCCGA 3562
Qy 2164 CCGAGATTTTTCATTCCTGCTGCTTATCCCTCAGTATTTAGCGAGGAAGACGATGCA 2223
Db 3563 CCGGACATCCAGTGTCTCAGGAGCTGAGCTGAGGTGAAGAGGCGCCAGAGCGCTGCT 3622
Qy 2224 TTTTGGGAGCAGCGCTGTTGGAAAGCACTCTTCTTCACTCTCTGAGAGACTTTAT 2283
Db 3623 CTGTTGGGAGCAGTGGCTGTTGGAGAGCAGTGGTCCAGCTCTCTGAGCGGTTCTAC 3682
Qy 2284 GACCCGCTGCAAGGACAAAGTCTGTTGATGTTGATGTCAGAAAGAAATTTGAATGTACAG 2343
Db 3683 GACCCCTTTGGCAGGAAAGTCTGTTGATGGCAAGAAATAAAGCACTGAATGTTTCA 3742
Qy 2344 TGCTCGTTCCCAATAGCAATCTTCTCAGAGCCTGCTCTTCACTTCACGCAAT 2403
Db 3743 TGCTCGAGCACAACCTGGGATCGTGTCCAGAGCCCAATCTGTTGACTCGAGCT 3802
Qy 2404 GCTGAGAAACATCCCTTATGTTGCAACAGCCTGTTGTCATTTAGATGAGATCAAGAA 2463
Db 3803 GCTGAGAAACATTCCTTATGGAGACAACGCGGTTGTTGTCACAGGAAGAGATTGTGAGG 3862
Qy 2464 GCGCAATTCAGCAAAATATCCATTTCTTTTATTTGAAGTCTCCCTGAGAAATACACACA 2523
Db 3863 GCAGCAAGAGAGCGCAACATACATGCTTCTATCGAGTCACTGCTGCTTAATAATATAGCACT 3922
Qy 2524 CAAATTTGAGCTGAAGAGCAGCAGCTTTCTGGCGGCAGAAAACAAAGACTAGCTATTGCA 2583
Db 3923 AAAGTAGAGACAAAGAACTCAGCTCTGTTGGTGGCGCAGAAACAACGCTTGCATAGCT 3982
Qy 2584 AGGCTCTTCTCAAAAACCCAAATTTTATTTGTTGATGAGGCGCACTTCAGCCCTCGAT 2643
Db 3983 CGTCCCTTTTGAAGCAGCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGAT 4042
Qy 2644 AATGACAGTGAAGAGTGTTCAGCATGCCCTTTGATAAAGCCAGGACGGGAAGCATGC 2703
Db 4043 ACAGAAAGTGAAGAGTGTTCAGAGAGCCCTGCAAGAGAGGCGCAGAGAGGCGCAGCTGC 4102
Qy 2704 CTAGTGTCACTCAGAGGCTCTCTGCAATTTCAAGACGCGAGATTTGATGTTGTTCTGAC 2763
Db 4103 ATTGTGATGCTCACCGCTGTCCCAATCCAGAAATGCACTTAATAGTGTGTTTTCAG 4162
Qy 2764 AATGGAAGATTAAGAGCAAGAACTCATCAGAGCTCTCAGAGAAATCGAGACATATAT 2823
Db 4163 AATGGCAGAGTCAAGGAGCATGCGCATCGAGCTGCTGCGCAGAAAGGCGCTCTAT 4222
Qy 2824 TTTAAAGTTAGTGAATGCAGAGTCA 2848
Db 4223 TTTTCAATGCTCAGTGTCCAGGCTG 4247

RESULT 10
US-10-097-340-1
; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNARABAPU

```

/ APPLICANT: Sebastian HOERSCH
/ APPLICANT: Shubhangi KAMATKAR
/ APPLICANT: Steve G. KOVATS
/ APPLICANT: Rachel E. MEYERS
/ APPLICANT: Michael MORRISSEY
/ APPLICANT: Peter OLANDT
/ APPLICANT: Hai SEN
/ APPLICANT: Peter VEIBY
/ APPLICANT: Gordon B. MILLS
/ APPLICANT: Robert C. BAST, Jr.
/ APPLICANT: Karen LU
/ APPLICANT: Rosemarie SCHMANDT
/ APPLICANT: Xumei ZHAO
/ APPLICANT: Karen GLATT
/ TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
/ TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
/ FILE REFERENCES: MEI-030
/ CURRENT APPLICATION NUMBER: US/10/097,340
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: 60/276,025
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/325,149
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/276,026
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/324,967
/ PRIOR FILING DATE: 2001/09/26
/ PRIOR APPLICATION NUMBER: 60/311,732
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/325,102
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/323,580
/ PRIOR FILING DATE: 2001-09-19
/ NUMBER OF SEQ ID NOS: 363
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4643
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-097-340-1

Query Match          36.1%; Score 1030.2; DB 15; Length 4643;
Best Local Similarity 62.2%; Pred. No. 4.1e-269;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

QY      166  ATTATTGATGAAGAAACCCGCTGTAGATAACTTTTCCACAGCTCGATATAAACCTGATCC 225
DB      1523  ATAATTGATTAAGCCCAAGTATTGACAGCTATTTCGAAGAGATGGGCAACACGATAT 1582

QY      226  ATAGAAGGAACCTGTGGAAATTTAAAAATGTGTTCTTTCAATTATCCATCAAGACCATCTATC 285
DB      1583  ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTACCATCTCGAAAGAAGATT 1642

QY      286  AAGATTCGAAAGTCTGAAATCTCAGAAATTAAGTCTGGAGAGACAGTCGGCTGGTCGGT 345
DB      1643  AAGATCTGTGAAGGCTCTGAACCTTGAAGGTGCAGATGGGCGAGCGTGGGCCCTGGTTGGA 1702

QY      346  CTCAAATGGCAGTGGGAAGAGTACGGTACTCCAGCTCTCTGCAGAGGTTATATGATCCGGAT 405
DB      1703  AACAGTGGCTGTGGGAAGAGCAACACAGTCCAGCTGTATGACAGGCTCTATGACCCCA 1762

QY      406  GATGGCTTTATCATGCGTGGATGAGAAATGACATCAGAGCTTTAAATGTGCGGCAATATCGA 465
DB      1763  GAGGGGATGCTCAGTGTGTGATGGACAGGATATTAGGACCAATAAATGTAAGGTTTCTACGG 1822

QY      466  GACCATATTCGAGCTGGTTAGTCTCAGAGCCCTGTTTGTTCGGGACCAACCATCAGTAAACA 525
DB      1823  GAAATCAATTTGGTGTGGTGTGAGTTCAGGAACCTGTATGTTTCCACCAAGTAGCTGAAAA 1882

QY      526  ATCAAGATATGGAACGAGATGATGTGACTGTATGAAGAGATGGAGAGAGCAGCAAGGAAACA 585
DB      1883  ATTGCGTATGCGCGTGAATAATGTCACCATGAGATGAGATGAGAAAGCTGTCAAGGAAGCC 1942

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Db 3023 ATTCCATAGCAGAGTTGTTGAATGAAATGTTGCTGGACAGCACTGAAAGATAAG 3082
 Qy 1684 CAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAAGCTTTGGAGAAATATACGTACTATA 1743
 Db 3083 AAAGAACTTAGAAGTGTGGGAAGATGCTACTGAAGCAATAGAAATCTTCGAAACCGTT 3142
 Qy 1744 GTGTCAATTAACAGGGAAGAAAGCCTTCGAGCAAAATGATGAAGAGATGCTTCAGACTCAA 1803
 Db 3143 GTTCTTTGACTCAGGAGCAGAGTTTGACATATGATGCTCAGAGTTTGCAGGTACCA 3202
 Qy 1804 CACGAAATACCTCGAAGAAAGCAGATTAATGGAAGCTGTTATGCAATCAGCCATGCC 1863
 Db 3203 TACAGAAACTCTTTGAGGAAGCAGACATCTTTGGAATTAATTTCTTCCTTCACCCAGCA 3262
 Qy 1864 TTTATATATTGCTATGACGAGGTTTCGATTTGGAGCCTTAATTTAAATTCAGCTGGA 1923
 Db 3263 ATGATGATATTTCTATGCTGGATGTTTCGGTTTGGAGCCTACTTGGTGGACATAAA 3322
 Qy 1924 CGAATGACCCAGAGGCGATGTTCAATGTTTACTGCAATTTGCATATGGAGCTATGGCC 1983
 Db 3323 CTCATGAGCTTGAGGATGTTCTGTAGTATTTTCAGCTGTTGCTTGGTGCATGGCC 3382
 Qy 1984 ATCGGAAAGCGTCTGTTGGCTCCTGAATTTCCAAAGCCAAATCGGGGCTGGCAT 2043
 Db 3383 GTGGGCAAGTCAGTTCAATTTGCTCCTGACTATGCCAAAGCAGCAATATCAGCAGGCCAC 3442
 Qy 2044 CTGTTTGGCTTTGTTGAAAGAAACCAATATACAGACGCGCAGTCAAGAGGGAAGAAAG 2103
 Db 3443 ATCATCATGATCATTTGAAAGAAACCCCTTTGATTGACAGCTACAGCAGGAGGCTAATG 3502
 Qy 2104 CCAGACATGTAAGGGAATTTAGAGTTTCGAGAGTCTTCTTCTTCTATCCATGTGCG 2163
 Db 3503 CCGAACAATTTGGAAGGAAATGTACATTTGGTGGATGTTGATTTCAACTATCCACCCGA 3562
 Qy 2164 CCAGATGTTTTCATCTCCGCTGGCTTATCCCTCAGTATTGAGCGAGGAAAGACAGTAGCA 2223
 Db 3563 CCGGACATCCAGTGTCTCAGGACTGAGCTGGAGTGAAGGAGGCGCAGACCTGGCT 3622
 Qy 2224 TTTGTGGGAGCAGCGCTGTGGGAAAGCACTTCTGTTTCAATTTCTGCGAGACCTTAT 2283
 Db 3623 CTGTTGGGACAGCTGCTGTGGGAAGACAGCTGCTCAGCTCTCTGGAGCGGTTCTAC 3682
 Qy 2284 GACCCGTCGAGACAGCTGCTGTTGATGTTGATGCTGATGCAAAAGAAATGAATGTACAG 2343
 Db 3683 GACCCCTTGGCAGGGAAGTCTGTTGATGGCAAGAAATGAAGCCACTGMAATGTTACG 3742
 Qy 2344 TGGCTCCGTTCCCAAAATAGCAATCGTTCTCAAGAGCTGTGCTTTCACTGAGCAAT 2403
 Db 3743 TGGCTCCGAGCACACCTGGGCATCGTGTCCAGGAGCCCATCTGTTTGAATGAGCAAT 3802
 Qy 2404 GCTGAGACATGCTGCTATGTTGACACAGCGCTGTGGTGCATTTAGATGAGATCAAGAA 2463
 Db 3803 GCTGAGAACATGCTGCTATGGAAGACACAGCGGCTGTGTCACAGGAGAGATTTGAGG 3862
 Qy 2464 GCCGCAATGAGCAAAATATCCTTCTTTTATGAAGGCTCTCCCTGAGAAATACACACA 2523
 Db 3863 GCAGCAAGGAGGCCAACATACATCGCTTCATGAGTCACTGCTCTAATAATATAGCACT 3922
 Qy 2524 CAAGTTGACCTGAAGGAGCAGCTTCTGGCGGCGAGAAAGCAAGAACTAGCTATTGCA 2583
 Db 3923 AAAGTAGAGACAAAGGAACCTCAGCTCTCTGGTGGCCAGAAACCAACGCAATGCGATAGCT 3982
 Qy 2584 AGGGCTCTTCTCCAAAGAACCCAAATTTATTTGATGAGGCACTTCAGCCCTCGAT 2643
 Db 3983 CGTGGCTTTGTAGACAGCTCATATTTGCTTTTGGATGAGCCACGTCAGCTCTGGAT 4042
 Qy 2644 AATGACGTAGAGGTTGGTTGACGATGCCCTTGTATTAAGCAGGACGGAGAGCATGC 2703
 Db 4043 ACAGAAAGTGAAGGTTGTCAAGAAAGCCCTGACAAAGCCAGAGAGGCGGACCTGC 4102
 Qy 2704 CTAGTGGTCACTCAGAGGCTCTCTGCAATTCAGAAAGCAGATTTGATGAGTGTCTGCAC 2763

Db 4103 ATTGTGATTGCTCACGCGCTGTCCACATCCAGAAATGCAGACTTAATAGTGTGTTTCAG 4162
 Qy 2764 AATGGAAGATTAAGGAACAGCAACTCATCAAGAGCTCTCAGAAATCGAGCATATAT 2823
 Db 4163 AATGGCAGAGTCAAGAGAGATGCGCATCAGCAGCTCTGCGCACAGAAAGSCATCTAT 4222
 Qy 2824 TTTAAGCTTAGTGAATGCACAGTCAG 2848
 Db 4223 TTTCAATGTCAGTGTCCAGGCTG 4247

RESULT 11
 US-10-007-926A-258
 ; Sequence 258, Application US/10007926A
 ; Publication No. US20030143539A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERTUCCI, FRANCOIS
 ; APPLICANT: HOULCAITE, REMI
 ; APPLICANT: BIRNBAUM, DANIEL
 ; APPLICANT: NGUYEN, CATHERINE
 ; APPLICANT: VIENS, PATRICE
 ; APPLICANT: FERT, VINCENT
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 ; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
 ; FILE REFERENCE: 1546-R-00
 ; CURRENT APPLICATION NUMBER: US/10/007,926A
 ; CURRENT FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,090
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 258
 ; LENGTH: 4643
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: atp-binding cassette, sub-family b
 ; OTHER INFORMATION: (mdr1ap), member 1 (ABCB1) gene.
 US-10-007-926A-258

Query Match 36.1%; Score 1030.2; DB 15; Length 4643;
 Best Local Similarity 62.2%; Pred. No. 4,1e-269;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

Qy 166 ATTATTGATAAGAAACCCAGATAGATAACTTTCCACAGCTGGATATAAAGCTGAATCC 225
 Db 1523 ATATTGATTAATAGCCAAAGTATTGACAGCTATTGAGAGTGGGCAAAACCATATAT 1582
 Qy 226 ATAGAAGGAACCTGGAAATTTAAATGTTCTTTCAATTTATCCATCAAGACCATCTATC 285
 Db 1583 ATTAGGGAAATTTGGAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAAAGAGTT 1642
 Qy 286 AAGNTTCTGAAGGCTCTGAATCTCAGAAATTAAGTCTGGAGACAGAGTCCCTTGGTCGGT 345
 Db 1643 AAGATCTTGAAGGCTCTGAACCTGAAGTGAAGTGGGCAACCGTGGCCCTGTTGGA 1702
 Qy 346 CTCAATGGCAGTGGGAAGATGACGGTAGTCCAGCTTCTGACAGGTTATATGATCCGGAT 405
 Db 1703 AACAGTGGCTGTGGGAAGAGCAACAGTCCAGCTGTATGACAGAGGCTCTATGACCCACA 1762
 Qy 406 GATGGCTTTATCATGTTGATGAGATGCAATCAGAGCTTTTAAATGTCGGCAATATATCA 465
 Db 1763 GAGGGGATGGTCAAGTGTGATGACAGAGGATATAGACCATAAATTAAGGTTTCTACGG 1822
 Qy 466 GACCATATTGAGTGTGTTAGTCAAGAGCCTGTTGTTTCGGGACCAACCATCATAGTAAAT 525
 Db 1823 GAAATCATTTGTTGTTGATGAGTCAAGAACTGTATTGTTTGGCCACCATAGTGTGAAAC 1882
 Qy 526 ATCAAGTATGGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
 Db 1883 ATTGCTATGTCGCTGAAATATGTCACATGATGATGATGATGATGATGATGATGATGAT 1942
 Qy 586 AATGCTGATGATTTTATCATGAGTGTTCCTAATAAATTTAATACATTTGTTAGGGGAAAA 645

[illegible]

3023	ATTGCAATACGAGGAGTTGTGTGAAATGAAATGTTGTTCTGGACAGCACTGAAAGATAAG	3082
1684	CAAGAACTTAAGCAATGCTGGAAAGATAGCAACTGAAAGCTTTGGAGAAATATACGTACTATATA	1743
3083	AAAGAACTAGAGGTGCTGGGAAGATCGCTACTTGAAGCAATAGAAAACCTTCGGAACCGTT	3142
1744	GTGTCAATTACAGGGGAAGAGCCTTCGACCAATGATGAGAGAGATGCTTCAGACTCAA	1803
3143	GTTCCTTTGACTCAGGAGCAGAAAGTTTGAACATATGTATGCTTCAGAGTTTTCAGAGTACCA	3202
1804	CACAGAAATACCTTCGAGAAAGCACAGATTATTGGAAGCTGTTATGCAITTCAGCCATGCC	1863
3203	TACAGAACTCTTTGAGGAAGCACACATCTTTGGAATTACATTTTCTTCACCCAGGCA	3262
1864	TTTATATATTTTGGCTATGACGAGGGTTTCGATTTTGGAGCCTTATTTAATCAAGCTGGA	1923
3263	ATGATGTATTTTCTTATGCTCGAATGTTCCGGTTTTGAGCCTTACTTGGTGGCACATAAA	3322
1924	CGAATGACCCAGAGGCGATGTTTCATAGTTTTTACTGCAATTGCAATGCAATGAGACTATGGCC	1983
3323	CTCATGAGCTTTGAGGATGTTCTGTGTAGTATTTTCACTGTGTCTTTGGTGCCATGGCC	3382
1984	ATCGGAAAAAGCTCGTTTTGGTCTCTGTAATATTCAAAGCCAAATCGGGGGCTGGCAT	2043
3383	GTGGGCAAGTCACTAGTTTCTGATATGCTGCAATATGCCCCAAAGCCAAAATATCAGCAGGCCAC	3442
2044	CTGTTTCCCTTGTTCGAAAGAAACCAATATATAGACAGCGCAGTCAAGAGGGAAGAAAG	2103
3443	ATCATCATGATCATGAAAGAAACCCCTTTTGATTTGACAGCTACAGACGGAAGCCTTAATG	3502
2104	CCAGACATGTCGAAGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTTCTATCAATGTGCG	2163
3503	CCGAAACATTTGGAAGGAATGTACATTTTGGTGAAGTTGTTATTCAACTATCCCACCGCA	3562
2164	CGAGATGTTTTCACTCTCGTGSCITTTATCCCTCAGTATTTGAGCGAGGAAGACAGTAGCA	2223
3563	CCGGACATCCAGTGTCTCAGGGACTGAGCCTGGAGGTGAAGAGGGCCAGACGCTGGCT	3622
2224	TTTGTGGGAGCAGCGGCTGTGGAAAAAGCACTTCGTTCAACTCTTCGACAGACTTTTAT	2283
3623	CTGTTGGCAGCAGTGCTGTGGGAAGACACAGTGGTCCAGCTCTCTGGAGCGTTCTTAC	3682
2284	GACCCGTGCAAGGACAAGTGTCTGTTTGTGATGTTGGATGCAAGAAATTTGAATGTACAG	2343
3683	GACCCCTTGGCAGGGAAGTGTGCTTGTATGTCGCAAGAAATTAAGCGCATGGAATGTTCAG	3742
2344	TGCTCGTCTCCAAATAGCAATCGTTCTCAAGAGCCTGTGCTCTTCAACTTCGACGCAAT	2403
3743	TGCTCTGAGCACACCTGGGCHTGTGTCTCCAGGAGCCCATCTCTGTTTCACTTCGACAT	3802
2404	GCTGAGACATCGCTTATGGTGACAAACAGCCGTGTGGTGCCATTTAGATGAGATCAAAGAA	2463
3803	GCTGAGAAATTTGCCCTTATGGAGAACACAGCCGGTGGTGTACAGGAAGAGATTTGTGAG	3862
2464	GCGCAAAATGCGCAAAATATCAATCTTTTATTGAGGTCTCCCTCGAGAAATACAAACACA	2523
3863	GCAGCAAGAGGCGCAACATATCATGCTTTCATGAGTCACTGCCCTTAATTAATATAGCACT	3922
2524	CAAGTTTGGACTGAAGGAGCAGACTTTCTCGCGGCCAGAAACAAAGACTAGCTATTGCA	2583
3923	AAAGTAGGAGACAAAGGAACCTCAGCTCTCTGTGGGCCAGAAACAAAGCATTTGCCATAGCT	3982
2584	AGGGCTCTTCTCCAAAACCCAAAATTTTATTGTTGGATGAGGCCACTTTCAGCCCTCGAT	2643
3983	CGTGCCCTTTGTAGACAGCTCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGAT	4042
2644	AATGACAGTGGAAGGTGTTTCAGCATGCCCCTTTGATTAAGCCAGGACGGGAAGGACATGC	2703
4043	ACGAAAGTGAAAGGTTGTGCCAAGAGCCCTGGACAAAGCCAGAGAGGCGCCGACCTGC	4102
2704	CTAGTGGTCACTCAAGGCTCTCTGCAATTTCAAGACGAGATTTCAATAGTGGTTCTGCMC	2763
4103	ATTGTAITGCTTCACGGCTGTCCACCAATCCAGAAATGCAGACTTAATAGTGTGTTTCAG	4162

QY 2764 AATGGAAGATTAAGGACCAAGGAATCATCAAGAGCTCTGAGAAATCGAGACATATAT 2823
 Db 4163 AATGGCAGATCAAGGAGCATGGACGCTCAGAGCTGCTGGCAGAGAAAGGCTCTAT 4222
 QY 2824 TTTAAGTTAGTAATGCACAGTCAG 2848
 Db 4223 TTTTCAATGGTCACTGCTCCAGGCTG 4247

RESULT 12

US-10-641-643-1167
 ; Sequence 1167, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; Susan G. Stuart
 ; Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCVTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/641,643
 ; FILING DATE: 14-Aug-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: <Unknown>
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1167:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g187468
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :

Query Match 36.1%; Score 1030.2; DB 17; Length 4646;
 Best Local Similarity 62.2%; Pred. No. 4.1e-269;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
 QY 166 ATTATGTATAGAAACCCAGTATAGATAACTTTTCCACAGCTGGATATAAACCTGAAATCC 225
 Db 1526 ATATTGATTAATAGCCCAAGTATTGACAGCTATTGGAAGAGTGGGCAACAAACAGATAAT 1585
 QY 226 ATAGAGCAACTGGGAATTTAAATATGTTCTTTCATTTATCCATTCAGACCATCTATC 285
 Db 1586 ATTAGGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTT 1645
 QY 286 AAGATTCTGAAGGTCGATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTGGTGGT 345

Db 1646 AAGATCTTGAAGGGCTGAACCTGAAGGTGCAGAGTGGGCAGACGGTGGCCCTGGTTGA 1705
 QY 346 CTCATATGCGAGTGGGAAGAGTACGGTAGTCCAGCTTCTGACAGGTTATATATATATATAT 405
 Db 1706 AACAGTGGCTGTGGGAAGGCAACAGCTCCAGCTGATGACAGAGGCTCTATGACCCCA 1765
 QY 406 GATGGCTTTATCATGGTGGATCAGAAATGATCATGAGCTTTTAAATGTGGCGATTTATCA 465
 Db 1766 GAGGGGATGGTCAATGTTGATGGACAGGATATTAGACCATAAATGTAAGGTTTCTACGG 1825
 QY 466 GACCATATTTGGAGTGGTTAGTCAAGAGCCTGTTTCTGGGACCAACCATCATGTAACAT 525
 Db 1826 GAAATCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1885
 QY 526 ATCAAGTATGGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
 Db 1886 ATTGCTATGGCGGTGAAATGTCACATGATGATGATGATGATGATGATGATGATGATGATG 1945
 QY 586 AATGCTATGATTTATCATGGAGTTCCTTAATAAATTTAATACATGTTGATGGGNAARA 645
 Db 1946 AATGCTATGATTTATCATGAACTGCTCATAAATTTGACACCTGGTGGAGAGA 2005
 QY 646 GAGCTCAAAATGATGGAGGCGAGAAACAGAGATCGCAATTCCTCGTCCCTTAGTTCGA 705
 Db 2006 GGGGCCAGTTGAGTGGTGGGAGAGAGAGATGCGCATTTGCATGCTGCCCTGGTTGCG 2065
 QY 706 AACCCCAAGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
 Db 2066 AACCCCAAGATTTCTCTGCTGATGAGGCGACGTCAGCCTTGGACACAGAGAGCGAAGA 2125
 QY 766 GCTGTTCAAGCTGCACTGAGAGAGGCGAGAAAGGTCGAGCTACAAATCTGCTGGTAGCAC 825
 Db 2126 GTGGTTCAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2185
 QY 826 CGACTTTTCTATTCGAAAGTCAGATTTGATGATGATGATGATGATGATGATGATGATGATG 885
 Db 2186 CGTTTGTCTACAGTTCGTAATGCTGAGCTCATCGCTGGTTCGATGATGAGGATCATTTG 2245
 QY 886 GAGAGAGGAGCAGATCTGAACTTAATGCGCAACAGAGCTCTATATTTATTCATCTGTGATG 945
 Db 2246 GAGAGAGGAAATCATGATGAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2305
 QY 946 TCAAGGATATTTAAAGAGCTGATGAACAGATGAGTCAATGACATATTTCTA----- 997
 Db 2306 ATGCAGACAGCAGGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2365
 QY 998 -----CTGAAAGAGAGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1045
 Db 2366 ATTGATGCTTGGAAATGCTTCAAAATGATTCAGATCCAGTCTAATAAGAAAAAGATCA 2425
 QY 1046 -----AGTCAGACTTCAITTCAGAGGCTGAGGAATCCACCCCAATCT 1086
 Db 2426 ACTCGTAGGAGTGTCCGTGGATCACAAGCCCAAGACAGAGAGCTTAGTACCAAGAGGCT 2485
 QY 1087 AAAGAGATAGTCTCTGAGTCTCTCTATTAATAATTTTAAAGTTAAACAGCTGAA 1146
 Db 2486 CTGGATGAAGATATACCTCCAGTTTCTTTTGGAGGATTTATGAAGCTAAATTTAACTGAA 2545
 QY 1147 TGGCTTTTGTGGTCTGGGACATTTGGCTTCTGTTCTAAATGGAATCTGTCATCCAGTA 1206
 Db 2546 TGGCTTTATTTTGTGGTGTATTTTGTGCAATTTATTAATGAGGCTCTGCAACCCAGCA 2605
 QY 1207 TTTTCCATCATCTTGGCAAAATTAACCAATGTTGGAAATTAATGATTAATAACCAATTA 1266
 Db 2606 TTTGCAATAATATTTTCAAGATTTATAGGGGTTTTTACAGAAATGATGATGATGATGATGAT 2665
 QY 1267 AAG---CATGATGCAGAAATTTATTCATGATATTCGTCAATTTGGTGTGTTATTTGCTTT 1323
 Db 2666 AAAGCAGATAGTAACTTTTTCATTTTCTAGCCCTTGGAAATTTATTTCTTTT 2725
 QY 1324 GTGATTTATTCAGGAGGATTTATTTACGGCAGAGAGGGAATTTTAAACGATGAGA 1383
 Db 2726 ATTACATTTTCTCTCAGGGTTTCAATTTGGCAAGCTGGAGATCTCTCACAAGCGG 2785

QY 1384 TTAAAGACACTTGGCCCTTCAAGGCAATGTTATATCAAGATATTCCTGGTTTGATGAAAG 1443
 Db 2786 CTCGATACATGTTTCCGATCCATGCTCAGACAGGATGAGTTGGTTTGATGACCT 2845
 QY 1444 GAAACAGACAGAGGCTTGCACAAATATTAGCCATATATAGCAAAATTCAGGA 1503
 Db 2846 AAAAAACCACTGAGCAATTTGCTACAGGCTGCCAATATGCTCTCAAGTTAAGGG 2905
 QY 1504 GCAACAGGTTCCAGGATGCGCTTTAAACACAAATATGCAACTAACATGGGACTTTTCAGTT 1563
 Db 2906 GCTATAGTTCCAGGCTTGGTAAATTAACCAATATATGCAAAATCTTGGGACAGGATA 2965
 QY 1564 ATCAATTCCTTTATATGATGGAGATGACATTCCTGATCTGATATTCCTCAGTA 1623
 Db 2966 ATTATATCCTTTCTATGTTGGCACTAACTGTTACTCTTAGCAATTTGACCCATC 3025
 QY 1624 CTTGCCCTGACAGGAATGATTGAAACCGCAGCAATGACTGGAATTTGCCAACAAAGATAAG 1683
 Db 3026 ATTGCAATAGAGGATTTGTAATGAAATGTTGCTGCAACAGCACTGAAAGATAAG 3085
 QY 1684 CAGAACTTAAGCATGCTGGAAGATAGCAACTGAGCTTTGGAGATATATGCTACTATA 1743
 Db 3086 AAGAACTAGAGGCTGCTGGAAGATGCTACTGAGCAATAGAAATTTCCGAACCGTT 3145
 QY 1744 GTGTCAATTAACAGGGAAGGCTTCGAGCAATGATGAGAGATGCTTCAGACTCAA 1803
 Db 3146 GTTCTTCTGACTCAGGAGCAGAGTTTGAACATATATGCTCAGAGTTTGCAGSTACCA 3205
 QY 1804 CACAAATACCTCGAAGAAAGCAGATTTATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
 Db 3206 TACAGAACTCTTTGAGGAAGCAGACATCTTTGGAATTAATTTCTTCAACCCAGGCA 3265
 QY 1864 TTTATATTTGCTGATGAGAGGCTTTCGATTTTCGAGCCCTATTTAATTCAGCTGGA 1923
 Db 3266 ATGATGATTTTCTTATGCTGATGTTTCCGGTTTGGAGCTACTTTGGTGGCAGATATA 3325
 QY 1924 CGAATGACCCAGAGGCGATGTTCAATGATTTTACTGCAATTTGATGAGCTATGGCT 1983
 Db 3326 CTCATGAGCTTTGAGGATGTTCTGTAGTATTTTCAGCTGTTGCTTTGGTGCATGCC 3385
 QY 1984 ATCGGAAAGCGCTGTTTGGCTGCTGATTTTCCAAAGCCAAATCGGGGCTGGCAT 2043
 Db 3386 GTGGGGCAAGTCAGTTCAATTTGCTGCTGACTATGCCAAAGCCAAATATCAGCAGGCCAC 3445
 QY 2044 CTGTTTGCCTTTGGAAGAAAGCAAAATATAGACAGCGCGCTCAAGAGAGGGAAG 2103
 Db 3446 ATCATCATGATCATTTGAAAGAAACCCCTTTGATTCAGAGCTACAGCAGGAGGCTTAATG 3505
 QY 2104 CCAGACATGTAAGGGAATTTAGAGTTTGAAGATCTCTTTCTTCTATTCATGTCGC 2163
 Db 3506 CCGAACCAATTTGGAAGGAATGTCAATTTTGTGAGTTGTTATTTCAACTATCCACCCGA 3565
 QY 2164 CCAGATGTTTTCATCTCCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAGACAGTAGCA 2223
 Db 3566 CCGACATCCAGTGCTTTTCCAGGACTGAGCTGAGGTTGAGAGGGCCAGCCTGGCT 3625
 QY 2224 TTTGTTGGGAGCAGCGCTGTGGGAAAGCACTTTCTGTTCAACTTTCTGAGAGACTTTAT 2283
 Db 3626 CTGTTGGGACAGTGCTGTGGGAAAGCAGCTGCTCAGCTCTCTGGAGCGGTTCTAC 3685
 QY 2284 GACCCGTCGAGGCAAGCTGTTTGTGCTGATGCAAGAGATTTCAATGTTACAG 2343
 Db 3686 GACCCCTTGGCAGGGAAGTCTGCTGATGCGCAAGAAATTAAGCGCACTGAAATGTTTCAG 3745
 QY 2344 TGGTCTCCCTTCCCAATAGCAATGTTCTTCAAGAGCGCTGTGCTTTCACTGAGCAATT 2403
 Db 3746 TGCTCCGAGCAGCACTTGGCATCGTGTCCAGGAGCCCATCTGTTTGTGCTGAGCAATT 3805
 QY 2404 GCTGAGACATGCTCTATGTTGACAAAGCGCTGTGTTGCCATTTAGATGATCAAGAA 2463
 Db 3806 GCTGAGACATGCTCTATGTTGAGCAACAGCGCGGTGTGTACAGGAGAGATCGTGAGG 3865

QY 2464 GCCGCAATGACGCAAAATATCCATTTCTTTTATTGAAGGTCTCCCTCAGAAATACACACA 2523
 Db 3866 GCAGCAAGGAGGCGCAACATACATCCTTCTCATGAGTCACTCCCTTAATAATATAGCAT 3925
 QY 2524 CAAATTTGAGCTGCAAGGAGCAGCTTTCTGCGCGCCAGAAACAAAGACTAGCTATTGCA 2583
 Db 3926 AAGATGAGGACAAAGGAACTCAGCTCTCTGTTGCGCCAGAAACAAAGCAATGCCATAGCT 3985
 QY 2584 AGGCTCTTCTCCAAAAACCCAAATTTTATTGTTGGATGAGCCACTTCAGCCCTCGAT 2643
 Db 3986 CGTGCCCTTTGTTAGACAGCCTCATATTTTGTCTTTTGGATGAGCCAGCTCAGCTCTGGAT 4045
 QY 2644 AATGACAGTGAAGAGTGTGTTCCAGCATGCCCTTGAATAAGCCAGGACCGGAAAGGACATGC 2703
 Db 4046 ACAGAAAGTGAAGAGTGTGTTCCAGAGGCCCTTGGACNAAGCCAGAGAGAGGCCGACCTGC 4105
 QY 2704 CTAGTGGTCACTCAGAGGCTCTCTGCAATTCAGACAGAGTTTGTATGATGTTCTGTCAC 2763
 Db 4106 ATTGTGATTTGCTCAGCGCTGTTCCACCATCCAGAAATGCAGACTTAATAGTGGTTTCAG 4165
 QY 2764 AATGGAAGATAAAGGAACAAGAACTCATCAAGAGCTCTCTGAGAAATCGAGACATATAT 2823
 Db 4166 AATGCGAGTCAAGAGCATGCGACGATCAGCAGCTCTCTGCGACAGAAAGGCACTAT 4225
 QY 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
 Db 4226 TTTTCAATGCTCAGTGTCCAGGCTG 4250

RESULT 13

US-10-343-657-1
 ; Sequence 1, Application US/10343657
 ; Publication No. US20040086882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roninson, Igor B.
 ; APPLICANT: Ruth, Adam
 ; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its
 ; TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs
 ; FILE REFERENCE: 00,616-A
 ; CURRENT APPLICATION NUMBER: US/10/343,657
 ; CURRENT FILING DATE: 2003-10-17
 ; PRIOR APPLICATION NUMBER: 60/222,313
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (425) ..(4264)
 US-10-343-657-1

Query Match 36.1%; Score 1030.2; DB 17; Length 4646;
 Best Local Similarity 62.2%; Pred. No. 4,1e-269;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

QY 166 ATTAATTGATAAGAAACCCAGTATAGATAAATTTTCCACAGCTGGATATAAACCCTGATCC 225
 Db 1526 ATAAATTGATAAATAAGCCAGTATTCAGACTATTTCGAGAGTGGGACAAACAGATAAT 1585
 QY 226 ATGAGAGGACTGTGGAATTTAAATTTTCTTCAATTTATCCATCAAGACCATCTATC 285
 Db 1586 ATTAAGGGAATTTGGAATTCAGAAATTTTCACTTCAGTTACCACTTCGAAAAGAGTT 1645
 QY 286 AAGATCTGAAAGCTCTGAATCTCAGAAATTAAGTCTGGAGAGACAGTGGCTTGGTCGGT 345
 Db 1646 AAGATCTTGAAGGCTTGAACCTGAAGTGCAGAGTGGGACAGCGTGGCTGGTTGGA 1705
 QY 346 CTCAATGGCAGTGGGAAGAGTAGGTAGTCCAGCTTCTCCAGAGGTTATATGATCCGGAT 405
 Db 1706 ARCAGTGGCTGTGGGAAGAGCAACAGTCTCAGTGTGAGAGGCTCTATGATCCCAACA 1765

QY 406 GATGCTTTATCATGTTGATGAGAAATGACATCAGAGCTTTAAATGTGCGGCAATTATCGA 465
Db 1766 GAGGGGATGGTTCAGTGTGATGGAACAGGATATTAGGACCAATAATGTAAGGTTTCTACGG 1825
QY 466 GACCATATGGAGTGGTGTAGTCAAGAGCTGTTTTGTTGGGACCAACATCAGTAACAAAT 525
Db 1826 GAAATCATTTGGTGTGGTGTAGTCAAGAGCTGTAATGTTTGGCCACCACCATAGCTGAAAC 1885
QY 526 ATCAAGATATGACGAGATGATGTGACTGATGAAGAGATGGAGAGCAGCAGGAAGCA 585
Db 1886 ATTGCTATGGCGGTGAAATGTCACCATGGATGAGATGGAAGAGCTGTCAAGGAGGCC 1945
QY 586 AATGGTATGATTTATCATGAGGTTTCTATTAATTAATTAATTAATTAATTAATTAATTA 645
Db 1946 AATGGCTATGATTTATCATGAATCTGGCTCAATAATTTGACACCTGGTGGAGAGAGA 2005
QY 646 GGAGCTCAAAATGAGTGGAGGAGGAGGAGGATCGCAATTTGCTGCTGCTTACTTCTGA 705
Db 2006 GGGGCCCATGAGTGGTGGGAGAGGAGGAGGATCGCAATTTGACAGTGGCTGCTTCTGC 2065
QY 706 AACCCCAAGATTCGATTTTGAATGAGGCTAGCTCTGCCCTGGATTCAGAAAGCAAGTCA 765
Db 2066 AACCCCAAGATTCCTGCTGATGAGGCGACGCTCAGCCTTGGACACAGAAAGCGAAGCA 2125
QY 766 GCTGTTCAAGCTGCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
Db 2126 GTGGTTCAAGTGGCTCTGATTAAGGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2185
QY 826 CGACTTTCTACTATTCGAATGCGAGTTTGAATTTGACCCCTAAAGATGGAATGCTGGCG 885
Db 2186 CGTTTGTCTACAGTTCGTAATGCTGACGTCATCGCTGGTTTCGATGATGAGTCAATGTG 2245
QY 886 GAGAGAGGAGCAGCTGCAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
Db 2246 GAGAAAGGAAATCATGATGAATCTCATGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 2305
QY 946 TCACAGGATATTAAGAAAGCTGATGAACAGAGTGGAGTCAATGACATATTCCTA ----- 997
Db 2306 ATGCAGACAGCAGGAAATGAGTTGAAATTAGAAATGACAGTGTGATGATCCAAAGTGAA 2365
QY 998 -----CTGAAGAAAGACCACTCACTTCTCTGCACTCTGTGAGAGCATCA--- 1045
Db 2366 ATTGATGCTTGGAAATGCTTCAATGATTTCAAGATTCAGTCTTAATGAAGAAAGATCA 2425
QY 1046 -----AGTCAGACTTCAATGACAGGCTGAGGAATCCACCAATCT 1086
Db 2426 ACTGTTAGAGTGTCTGATGATCAAGCCAGACAGAGGCTTAGTACCAAGAGGCT 2485
QY 1087 AAAGAGATAGTCTCTGAGGCTCTCTAATTAAGAAATTTAAAGTTAAAGAGGCTGAA 1146
Db 2486 CTGGATGAAGATATACCTCCAGTTTCTTTTGGAGGATTTATGAAGCTTAAATTTAACTGAA 2545
QY 1147 TGCCCTTTTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1206
Db 2546 TGCCCTTTTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2605
QY 1207 TTTTCCATCATCTTTGCAAAATTTAATCAATGTTTGGAAATTAATGATTAAGCCATTA 1266
Db 2606 TTTGCAATAATATTTCAAGATTTAGGGGTTTTCAGAAATTTGATGATCTGGAACA 2665
QY 1267 AAG---CATGATGCAAAATTTATCCAGATATTCGTCATTTGGGCTGTATTTGCTTT 1323
Db 2666 AAGCAGAAATGATGATCTGTTTCACTATTTGTTTCTAGCCCTTGGAAATTTATTTCTTT 2725
QY 1324 GTCAGTATTTCAAGGAGGATTTTATGCGCAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAG 1383
Db 2726 ATTACATTTTCTCAGGAGTTTCAATTTGGCAAGGCTGGAGAGATCTCCACCAAGCGG 2785
QY 1384 TTAAGACATCTGSCCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1443
Db 2786 CTCGATACATGTTTTCGATCTCAGACAGGATGTGAGTTGGTTTGTGATGACCT 2845

QY 1444 GAAAAAGGACAGAGGCTTTGACAAACAAATATTAGCCATAGATATAGCACAAATTTCAAGGA 1503
Db 2846 AAAAAACCCACTGGAGCATTTGACTACAGGCTGCCAATGATGCTGCTCAAGTTAAAGGG 2905
QY 1504 GCAACAGGTTCCAGGATTTGGGCTTTAAACAAAAATGCAAACTAAACATGGGACTTTCAAGTT 1563
Db 2906 GCTATAGTTCCAGGCTTGTCTGTAATTTACCAGAAATATAGCAAACTTTGGGACAGGAATA 2965
QY 1564 ATCATTTCTTTATATATGATGAGGAGATGACATTTCTGATTTCTGAGTATTTGCTCCAGTA 1623
Db 2966 ATTATATCTTTCTATCTATGTTGGCACTAACTGTTTCTTATGAGAAATTTGATACCATC 3025
QY 1624 CTTGCGGTGACAGGAATGATTGAAACCGCAGCAATGACTGGATTTGCAACAAAGATAAG 1683
Db 3026 ATTGCAATFAGCAGGATTTGTAATGAAATGTTGTTGTCGACAACTGCAAGATAAG 3085
QY 1684 CAAGAACTTAAGCATGCTGGAAGATAGCAACTGAGCTTTGGAGATATACGTACTATA 1743
Db 3086 AAAGAACTAGAGGCTGCTGGAGATGCTACTGAAACAAATAGAAAACTTTCCGAACCGTT 3145
QY 1744 GTGTCATTAAACAGGGAAGAAAGCCCTTCAGCAATGATGAAGAGATGCTTTCAAGCTCAA 1803
Db 3146 GTTCTTTGATCTCAGGAGCAGAGTTTGAACATATGATGCTCAGATTTGCAAGTACCA 3205
QY 1804 CACAGAAATACCTCGAAAGAAAGCAGATTAATGGAAGCTGTTATGCAATTCAGCATGCCC 1863
Db 3206 TACAGAAACTCTTTGAGGAAAGCACAATCTTTGGAAATTAACATTTTCTTCCACCCAGCA 3265
QY 1864 TTTATATTTTGGCTATGACAGAGGCTTTGATTTGGAGCTTATTAATTTCAAGCTGGA 1923
Db 3266 ATGATGATTTTCTTATGCTGATGTTTCGGTTTGGAGCTTACTTTGGTGGCACAATAA 3325
QY 1924 CGAATGACCCAGAGGAGCTATTTATAGTTTCTACTGCAATTTGCAATTTGAGAGCTATGGCC 1983
Db 3326 CTGATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAGCTGTTGCTTTGGTGGCATGGCC 3385
QY 1984 ATCGAAAAACGCTGCTTTTGGCTCTGTAATTTCCAAAGCCAAATCGGGGCTGGCCAT 2043
Db 3386 GTGGGCAAGTCAGTTCAATTTGCTCTGACTATGCCAAAGCCAAATATCAGAGCCAC 3445
QY 2044 CTGTTGCTCTTTTGGAAAAAGAAACCAAAATATAGACGCGCAGTCAAGAGGGAAGAAAG 2103
Db 3446 ATCATCATGATCAATTTGAAAGAAACCCCTTTGATTTGACAGCTACAGACGGAAGGCTAATG 3505
QY 2104 CCAGACATGTTGAAGGAAATTTAGAGTTTCGAGAGCTCTTTCTTTCTATCCATGTCG 2163
Db 3506 CCGAACCAATTTGAAGGAAATTTGTCATTTGGTGAAGTTGTTCACTATTTCCACCCGGA 3565
QY 2164 CCAGATGTTTTCATCTCCGCTGCTTATCCCTCAGTATTCAGCGAGGAAAGACAGTAGCA 2223
Db 3566 CCGACATCCAGTCTTTCAGGACTGAGCTGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAG 3625
QY 2224 TTTGGGGAGCAGCGCTGTGGGAAAGCAGCTTCTGTTGAACTTTCTGAGAGACTTTAT 2283
Db 3626 CTGGTGGGAGCAGTGTGCTGTGGGAGAGCAGTGTGCTCCAGCTCTTGGAGCGGTTCTAC 3685
QY 2284 GACCCGTCAGAGCAGAGTCTGTTGATGCTGTGATGCAAAAGAAATTTGAAATGTTACAG 2343
Db 3686 GACCCCTTGGCAGGAAAGTCTGCTTGAATGGCAAGAAATTAAGCGCTGAATGTTTACAG 3745
QY 2344 TGGCTCTCCCTTCCCAATAGCAATCTTCTCAAGAGCTGTGCTCTTCACTCAGAGCAAT 2403
Db 3746 TGGCTCCGAGCACACCTGGGCTATGCTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3805
QY 2404 GCTGAAACATGCTGCTATGTTGACCAAGCGCTGTGCTGCTGCTATGATGAGATCAAGAA 2463
Db 3806 GCTGAGAACTTGTCTATGGAGACAGACGCGGGTGTGTACAGGAGAGATCTGTGAGG 3865
QY 2464 GCGCAATGTCAGCAAAATATCCATTTCTTTTATGAGAGTCTCCCTGAGAAATACAACACA 2523
Db 3866 GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3925
QY 2524 CAAGTTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2583

Db 3926 AAAGTAGGAGAGCAAGGAACTCAGCTCTCTGGTGGCCAGAAACACGCAATGCCATAGCT 3985
Qy 2584 AGGGCTTTCTCAAAAAACCCAAATTTTATTTGGATGAGGCGCACTTCAGCCCTCGAT 2643
Db 3986 CGTGCCCTTGTAGACAGGCTCATATTTTGGCTTTGGATGAAGCCACGTCAGCTCTGGAT 4045
Qy 2644 AATGACAGTGAGAGTGCTTCAGCATGCCCTTGATTAAGCCAGGACCGGAGAGGACATGC 2703
Db 4046 ACAGAAAGTGAAAGGTTTCCAAAGAGCCCTGGACAAAGCCAGAGAGGCGCGACCTGC 4105
Qy 2704 CTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAACCGCAGATTTGATAGTGGTTCTGCA 2763
Db 4106 ATTGTGATTGCTCACCGCTGCTCCACCATCCAGATCCAGACTTAATAGTGGTTTCAG 4165
Qy 2764 AATGGAAGATTAAGAAACAAAGAACTCATCAGAGCTCTGAGAAATCGACATATAT 2823
Db 4166 AATGGCAGAGTCAAGGAGCATGCGCATCAGCAGCTGCTGCGACAGAAAGCATCTAT 4225
Qy 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
Db 4226 TTTTCAATGGTCAATGTCAGGCTG 4250

RESULT 14
US-09-866-866A-1
; Sequence 1, Application US/09866866A
; Patent No. US2002010224A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 36.0%; Score 1028.6; DB 9; Length 3860;
Best Local Similarity 62.2%; Pred. No. 9.8e-289;
Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;
Qy 166 ATTATTGATAAGAAACCCAGTATAGATAAATCTTTCCACAGCTGGATATAAACCCTGAATCC 225
Db 1102 ATAAATTGATTAATAGCAAGTATTGACAGCTATTCGAGAGTGGGCAACCAAGATAAT 1161
Qy 226 ATGAGAGAACTGTGGAATTTAAATGTTCTTTTCATATTCATCATCAGACCAATCTATC 285
Db 1162 ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTTACCCTATCTCGAAAGAAGTT 1221
Qy 286 AAGATTCTGAAAGCTCTGAATCTCAGAAATTAAGTCTGGACAGACAGTGGCTTGGTCGGT 345
Db 1222 AAGATCTTGAAGGCTCTGAACCTGAAGTTCAGAGTGGGCGAGCGGTGGCTTGGTGA 1281
Qy 346 CTCAATGGCAGTGGGAAGATGACGTTAGTCCAGTCTTCAGAGGTTATATGATTCGGAT 405
Db 1282 AAGAGTGGCTGTGGGAAGAGCAACAGTCCAGTCCAGTCTGATGCAAGAGGCTCTATGACCCCA 1341
Qy 406 GATGCTTTTATCATGGTGGATGAGATGACATCAGAGCTTTAAATGTGGCGCATTTATCGA 465
Db 1342 GAGGGGATGCTAGTGTGTGAGGACAGATATTAGGCCAATAATGTAAGGTTTCTACGG 1401

Qy 466 GACCATATTGAGTGGTTAGTCAAGAGCGCTGTTTGTTCGGGACCCACCATCAGTAACAAT 525
Db 1402 GAATCAATTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1461
Qy 526 ATCAAGTATGACGAGATGATGTGATGAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
Db 1462 ATTGCTATGCGCGTGAATGTCAACATGATGAGATTTGAGAAAGCTGTCAAGAGAGGCC 1521
Qy 586 AATGGTATGATTTTATCATGAGTTTCTTAATAAATTTAATATCATTTGGTAGGGGAAAAA 645
Db 1522 AATGCTATGATTTTATCATGAACTGCTCTTAATAATTTGACACCTGTTGGAGAGAGA 1581
Qy 646 GGAGCTCAATGAGTGGAGGAG 705
Db 1582 GGGGCCAGTTTGGTGGTGGGAG 1641
Qy 706 AACCCAGATTTCTGATTTTATGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
Db 1642 AACCCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1701
Qy 766 GCTGTTCAAGCTGCATCGAG 825
Db 1702 GTGGTTCAAGTGGCTCTGAGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1761
Qy 826 CGACTTTCTATTTGAGAGTGCAGATTTGATTTGAGACCTTAAGAGAGAGAGAGAGAGAGAG 885
Db 1762 CGTTTGTCTACAGTTCTGTAATGCTGACGTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1821
Qy 886 GAGAAAGCAGACATGCTGAACTAATGCAAAACGAGGTCTATATTTACATCTTGTGATG 945
Db 1822 GAGAAGGAAATCATGATGAACTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1881
Qy 946 TCACAGGATATTAAGAGAGTGAAG 997
Db 1882 ATGCAGACAGCAG 1941
Qy 998 -----CTGAAAG 1045
Db 1942 ATTGATGCTTGGAAATGCTTCAATGATTTCAAGATCAGTCTAATTAAGAAAGAGATCA 2001
Qy 1046 -----AGTCAGACTTCATGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
Db 2002 ACTCGTAGAGTGTCCGTGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2061
Qy 1087 AAAGAGATGAGTCTTCTGAGTCTCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146
Db 2062 CTGGATGAAGATATACCTCCAGTTTCTTTTGGAGAGATTAAGAGCTTAATTTAACTGAA 2121
Qy 1147 TGGCTTTTGTGCTTCTGGGAGACATTTGCTTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAG 1206
Db 2122 TGGCTTTTGTGCTTCTGGGAGACATTTGCTTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAG 2181
Qy 1207 TTTTCCATCATCTTTGCAAAATTAATACCATGTTTGGAAATTAATTAAGAGAGAGAGAGAGAG 1266
Db 2182 TTTGCAATAATATTTCAAGAGATTAAGAGAGATTAAGAGAGATTAAGAGAGATTAAGAGAGAG 2241
Qy 1267 AAG---CATGATGAG 1323
Db 2242 AAAG 2301
Qy 1324 GTGAGTTATTCATGAGAGAGATTTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
Db 2302 ATTACATTTTCTTCAAGGTTTCAATTTGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2361
Qy 1384 TTAAG 1443
Db 2362 CTCGAGATCATGTTTTCGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2421
Qy 1444 GAAAG 1503
Db 2422 AAAAG 2481
Qy 1504 GCAACAGGTTCCAGGATTTGGGCTTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1563

Db 2482 GCTATAGGTTCCAGGCTTCTGTATATCCCGAATATAGCAATCTTGGGACAGGAATA 2541
 Qy 1564 ATCAATTCCTTTATATATGATGGAGATGACATTCCTGATCTGAGTATTCCTCAGTA 1623
 Db 2542 ATTATATCCTTCATCTATGTTGGCAACTAACTACTGTTACTCTTAGCAATTTGATCCATC 2601
 Qy 1624 CTTCGCGTGAAGCAATGATTTGAACCCGACGAATGACTGCAATTTGCCAACAAAGATAAG 1683
 Db 2602 ATTGCAATAGCAGGAGTTTGTGNAATGAATGTTGTCTGGACAGCACTGAAGATAG 2661
 Qy 1684 CAAGAACTTAGCTAGCTGCTGGAAGATAGCACTGAGCTTTGAGGAATATACCTACTATA 1743
 Db 2662 AAAGAACTTAGAGGTGCTGGGAAGATGCTACTGGAAGCAATAGAAATCTTCGAACCGTT 2721
 Qy 1744 GTGTCAATTAACAAGGAAAGCCCTCCAGCAATATGATCAAGAGATGCTTCAGACTCAA 1803
 Db 2722 GTTCTTTGACTCAGGAGCAGAACTTTGAACAATGATGATGCTCAGAGTTTGCAGGTACCA 2781
 Qy 1804 CACGAATACCTCGAAGAAAGCAAGATTAATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
 Db 2782 TACAGAACTCTTTGGAAGAAAGCAACATCTTTGGAATTAACATTTCTTCACCCAGGCA 2841
 Qy 1864 TTATATATTTTGGCTATGACGAGGCTTTCGATTTGGAGCTTATTTAATTCAGCTGGA 1923
 Db 2842 ATGATGATATTTCTTATGCTGATGTTTCCGGTTTGGAGCTTACTTGTGGCAATATA 2901
 Qy 1924 CGAATGCCAGAGGCTGTTTCTAGTCTTTTACTGCAATTCATGAGCTATGGCC 1983
 Db 2902 CTCATGAGCTTTGAGGATGTTCTGTTAGTATTTTCACTGTTGCTTTGTGGCCATGGCC 2961
 Qy 1984 ATCGAAAGAGCTGCTTTGGCTCTGGAATATTTCCAAAGCCAAATCGGGGCTGCCAT 2043
 Db 2962 GTGGGCAAGTCAGTTCAATTTGCTCTGACTATGATGCAAGGCAATATATCAGAGCCAC 3021
 Qy 2044 CTGTTGCTGTTTGGAAAGAAACCAATATAGACGCGAGTCAAGAGGGAAGAAAG 2103
 Db 3022 ATCATCATGATCATTTGAAAGAAACCCCTTTGATGACAGCTTACAGCAGGAAGCCCTAATG 3081
 Qy 2104 CCAGACATGTAAGGGAATTTAGAGTTTCGAGAACTCTCTTTCTTATCCATGCTGC 2163
 Db 3082 CCGAACACATTTGAAGGAATGTCACATTTGGTGAAGTTGATTTCAATATCCACCCGA 3141
 Qy 2164 CCAGATGTTTTCATCTCCGTTGCTTATCCCTAGTATTCAGGAGGAAAGACAGTAGCA 2223
 Db 3142 CCGACATCCAGTCTTCAGGAGCTAGGCTCGGAGGAGAGGAGGAGGAGGAGGAGGAGG 3201
 Qy 2224 TTTGTGGGAGCAGCGCTGTGGGAAAGCACTTCTTGTTCAGCTTCTGAGAGACTTTAT 2283
 Db 3202 CTGTTGGGAGCAGTGTGCTGTGGAGAGCAGCAGTGTCCAGCTCTGAGCGGTTCTAC 3261
 Qy 2284 GACCCGCTGCAAGCAAGTGTCTGATGCTGTGATGCTGATGCAAGAAATGATGATAG 2343
 Db 3262 GACCCCTTGGCAGGAAAGTCTGCTTGTATGGCAAGAAATTAAGCGACTGATGTTTCA 3321
 Qy 2344 TGGCTCGGTTCCCAATAGCAATCGTTCTCAGAGGCTGTGCTCTTCACTGCGAGCAT 2403
 Db 3322 TGGCTCGGAGCACACCTGGGCACTGCTGCTCCAGAGGCCATCTCTTTGACTGCGAGAT 3381
 Qy 2404 GCTGAGAACTCGCTATGCTGCAACAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2463
 Db 3382 GCTGAGAACTCGCTATGAGAACACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3441
 Qy 2464 GCGCAATCAGCAATATCCATCTTTTATGGAAGGTCTCCCTGAGAAATACACACA 2523
 Db 3442 GCAGAAAGGAGGCCAACATACATGCTCTCATGAGTCACTGCTTAAATAATATAGCACT 3501
 Qy 2524 CAGTTGAGCTGAAGAGGAGCAGCTTTCTGGCGGCGCAGAAACAGTACTGCTATTGCA 2583
 Db 3502 AAGTAGAGACAAAGAACTCAGCTCTCTGTTGGCCAGAAACAGCAATTCCTCATGCT 3561
 Qy 2584 AGGCTCTTCTCCAAAGCCCAATTTTATTTGATGAGGCGCCACTTCAGCCCTCGAT 2643

Db 3562 CGTGCCCTTGTGTAGACAGCCCTCATTTTCTTTTGGATGAGACCCAGCTCAGCTCTGGAT 3621
 Qy 2644 AATGACAGTGAGAAAGGTGTGTTCAGCATGCTTTGATATAAGCCAGGAGGAGGAGCATGC 2703
 Db 3622 ACAGAAAGTGAAAGGTGTGTTCAGAAAGCCCTGGACAAAGCCAGAGAGGAGCCGACCTGC 3681
 Qy 2704 CTAGTGTCTACTCAGAGCTCTCTGCAATTCAGAAAGCGAGATTTGATAGTGTCTCTGCAC 2763
 Db 3682 ATTGTGATTGCTCAGCCCTGTCCACATCCAGATTCAGACTTATATAGTGTGTCTCAG 3741
 Qy 2764 AATGGAAGATTAAGGAAAGCAAGCAATCTATCAAGAGCTCTCTGAGAAATCGAGACATATAT 2823
 Db 3742 AATGGCAGAGTCAAGGAGCATGCGAGCATCAGCAGCTCTGCGCACAGAAAGGCACTTAT 3801
 Qy 2824 TTTAAGTTAGTGAATGACACAGTCAG 2848
 Db 3802 TTTTCAATGCTCAGTGTCCAGGCTG 3826

RESULT 15
 US-09-866-866A-3
 ; Sequence 3, Application US/09866866A
 ; Patent No. US20020102244A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sorrentino, Brian
 ; APPLICANT: Schuetz, John
 ; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
 ; FILE REFERENCE: 1340-1-021CIP2
 ; CURRENT APPLICATION NUMBER: US/09/866,866A
 ; CURRENT FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: 09/584,586
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/11825
 ; PRIOR FILING DATE: 1999-05-27
 ; PRIOR APPLICATION NUMBER: 60/086,988
 ; PRIOR FILING DATE: 1998-05-28
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 3860
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-866-866A-3

Query Match 36.0%; Score 1028.6; DB 9; Length 3860;
 Best Local Similarity 62.2%; Pred. No. 9.8e-269;
 Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

Qy 166 ATTAATTGATAAGAAACCCAGTATAGATACTTTCCACAGCTGGATATAAAACCTCAATCC 225
 Db 1102 ATTAATTGATAAGCAAGTATTTGACAGCTTATTCAGAGAGTGGGCAANACCAGATAAT 1161
 Qy 226 ATGAGAGGAACTGTGGAATTTTAAATGTTTCTTTCAATTAATCAATCAAGACCATCTATC 285
 Db 1162 ATTAAGGGAATTTGAATTCAGAAATGTTCACTTCACTTACCCATCTCGAAAAGAGTT 1221
 Qy 286 AAGATTTCTGAAAGGTCTGAATCTCAGAAATTAAGTCTGGAGAGACAGTCCCTTGTGCTGT 345
 Db 1222 AAGATTTGAAAGGCTTGAACCTGAAGTGGAGAGTGGGAGAGCGTGGCTGCTGTTGGA 1281
 Qy 346 CTCAATGGCAGTGGGAAAGTACGGTATGCTCAGCTTCTGAGAGGTTTATATGATCCGGAT 405
 Db 1282 AACAGTGGCTGTGGGAAAGAGCACAACAGTCCAGCTGATGAGAGGCTCTATGACCCACA 1341
 Qy 406 GATGCGCTTTATCATGTGTGATGAGAAATGATCAGAGCTTTTAAATGTGCGGCATTATCGA 465
 Db 1342 GAGGAGTGGTCACTGTTGATGGAAGGATATAGGACCAATTAATGTAAGGTTTCTACGG 1401
 Qy 466 GACCATATTTGGAGTGGTGTAGTCAAGAGCTGTTTGTGGGACCAACCATCAGTAAACAT 525
 Db 1402 GAAATCATTTGGTGTGAGTCAAGAAACCTGTATTTGTTGCGCACCAAGATAGCTGAAAC 1461
 Qy 526 ATCAAGTATGGACGAGATGATGTGACTGTATGAAGAGATGGAGAGAGCAGCAAGGAGCA 585

Db	1462	ATTGCGTATGCGCGTGAAAAATGTCACCATGSGATGAGATTGAGAAAGCTGTCAAGGAAGCC	1521
Qy	586	AATGCGTATGATTTATCATGGAGTTTCCTAAATAAATTTAATACATTTGGTAGGGGAAAAA	645
Db	1522	AATGCCATAGCTTTATCATGAACACTGCTCATAAATTTGCACACCTGGTTGGAGAGAGA	1581
Qy	646	GGAGCTCAAAATAGATGGAGGGCGAGAAACAGAGAGATGCAATGCTGTCGCTTAGTTTGA	705
Db	1582	GGGGCCAGATTGATGGTGGGCGAAGCAGCAGAGATGCCATTGCAGTGCCTGGTTGCG	1641
Qy	706	AACCCCAAGATCTGATTTTAGATGAGGCTACGCTGCGCTGGATTGAGAAACCAAGTCA	765
Db	1642	AACCCCAAGATCCCTCTGCTGGATGAGGCCACGTCAGCTTTGGACACAGAAAGCGAGCA	1701
Qy	766	GCTGTTTCAAGCTGCACCTGGAAGAGCGGAGCAAAAGGTCGGACTCAATPGTGGTAGCACAC	825
Db	1702	GTGTTTCAGGTGGCTCTGGATAGGCGAGAAAGGTCGGACCACTCATTTGTGATAGCTCAT	1761
Qy	826	CGACTTCTACTATTGCAAGTGCAGATTTGATTTGTGACCCCTAAGAGATGAAATGCTGGCG	885
Db	1762	CGTTTGCTACAGTTGCTAATGCTGAGCTCATGCTGGTTTCGATGATGAGTCATTTG	1821
Qy	886	GAGAAAGGAGCACATGCTGAACTAANTGCCAAAAAGAGGTCTATATTATTCACCTTGTGATG	945
Db	1822	GAGAAAGGAAATCATGATGAACATCATGAAGAGAAAGCGATTTACTTCAAACTGTGCACA	1881
Qy	946	TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTTCTA-----	997
Db	1882	ATGCAGACACAGCGAAATGAAGTTGAATTAGAAAAATGCACCTGATGAATCCAAAAGTGAA	1941
Qy	998	-----CTGAAAGAAAGACCAACTCACTTCTCTGCACTCTGTGGAAGAGCATCA--	1045
Db	1942	ATTGATGCCTTGGAATGTCTTCAAAATGATTCAGATCCAGTCTAATAAGAAAGATCA	2001
Qy	1046	-----AGTCAGACTTCATTGACAAAGCTGAGGATCCACCCCAATCT	1086
Db	2002	ACTCGTAGGAGTGTCCGTGGATCACAGCCCAAGACAGAAAGCTTAGTACAAAGAGGCT	2061
Qy	1087	AAAGAGATAAGTCTTCTGAAGTCTCTCTATTAAAAATTTTAAAGTTTAAACAAGCTGAA	1146
Db	2062	CTGGATGAAGATATACCTCCAGTTTCCTTTTGGAGGATTAAGAGCTTAATTTAATCTGAA	2121
Qy	1147	TGCGCTTTTGTGGTTCTGGGACATTTGGCTTCTGTTCTTAAATGGAACGTGTTCAACGTA	1206
Db	2122	TGGCTTATTTTGTGTGTGTGATTTTGTGCGCATTTATAATGAGGCTTGCACACGCA	2181
Qy	1207	TTTTTCCATCATTTTGCAGAAATTTATAACCATGTTTGGAAATAGTATAAACCAATTA	1266
Db	2182	TTTGCAATAATTTTCAAGATTTATAGGGTTTTTACAGAGATGATGATCTCTGAAACA	2241
Qy	1267	AAG---CATGATGCAGAAAAATTTATTCATGATATTGCTCATTTTGGGTGTTATTTCGTTT	1323
Db	2242	AAACGACAGAAATAGTAATCTGTTTCTACTATTGTTTCTAGCCCTTGGAAATTTTCTTTT	2301
Qy	1324	GTCHGTTATTTTCAGAGGATTTATTTTACGCGAGCAGCGGAAATTTTAAAGATGAGA	1383
Db	2302	ATTAACATTTTTCCTTCAAGGTTTTCATTTTGGCAAGCTGGAGAGATCTCTCAACAAGCGG	2361
Qy	1384	TTAAGACACTTGGCTTCAAGAGCATGTTATATCAGGATATTGCTCGTTTGTGATGAADAG	1443
Db	2362	CTCGATACATPGTTTTCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGTATGACCCT	2421
Qy	1444	GAAACACGACAGGAGCTTGACAAACAATATTAGCCATAGATATAGCACAAATTCAGGA	1503
Db	2422	AAAAACACCACTGGAGCATTTGACTATCCAGGCTCCGCAATGATGCTCAAGTTAAAGGG	2481
Qy	1504	GCACAGGTTCCAGGATTTGGCGTCTTAACACAAATGCAACTACACTACGAGCTTTTCAGTT	1563
Db	2482	GCTATAGTTCACGCTTGTGTAATTTACCCAGAAATAGCAAAATCTTGGACAGGATA	2541
Qy	1564	ATCATTTTCTTTTATATATGATGGAGATGACATTTCTCGATTCTGAGTATTGCTCCAGTA	1623

2542	ATTATATCCCTTCATCTACTATGGTTGGCAACTAAACACTGTTACTCTTAGCAATTTGACCCATC	2601	
Qy	1624	CTTCCCGTGACAGGAATGATTTGAAACCGCAGCAATGACCTGGATTTTGCCAAACAAGATAAG	1683
	2602	ATTGCAATAGCAGGATTTGTTGAAATGCAAAATGTTGTCTGGACAACGACCTGAAAGATAAG	2661
	1684	CAGAACCTTAAGCATCTCTGGAAAGATAGCAACTGAGCTTTGGAGAAATATAGTACTATA	1743
Db	2662	AAGAAGACTAGAAGTCTCTGGGAAGATCGCTACTGGAAGCAATAGAAAACCTTTCCGACCGTT	2721
	1744	GTGTCATTAAACAGGGAAAGAGCCITTCGAGCAAAATGATGAAGAGATGCTTCAGAGCTCAA	1803
	2722	GTWTTCTTGACTCAGGAGCAGAGTTTGAACATAATGATGCTCAGAGTTTGCAGGTACCA	2781
Qy	1804	CACAGAAATACCTCGAAGAAAGCACAGATATTTGGAGCTGTATTCATTGACCTCAGCCATGCC	1863
	2782	TACAGAAACTCTTTGAGAAAGCACACATCTTTGGAAATTACATTTTCTTTCAACCCAGGCA	2841
	1864	TTTATATATTTTCCCTATGCAGCAGAGGTTTTCGANTTTGGAGCCATTTAAATTCAGGCTGGA	1923
Db	2842	ATGATGTATTTTCTTATGCTGGATGTTTCCGGTTTGGAGCTTACTTGGTGGCACATAAA	2901
	1924	CGAATGACCCGAGGEGCATGTTTCATAGTTTTTATGCAATTTGCATATGAGAGTATGCGC	1983
	2902	CTCATGAGCTTTGAGGATGTTCTGTGTAGTATTTTCAGCTGTGTCTTTGGTGGCATGCGC	2961
Qy	1984	ATCGGAAAACGCTCGTTTGGCTCTCTGATATTTCCAAAGGCCAAATCGCGGGCTGCGCAT	2043
	2962	GTGGGCAAGTCAGTTTCATTTGCTCTCTGACTATGCCAAAGCCAAATATTCAGCAGGCCAC	3021
	2044	CTGTTTGCCTTGTTTGGAAGAAACCAAAATATAGACAGCGCGCAGTCAAGAAGGGAAAAAG	2103
Db	3022	ATCATCATGATCATTTGAAAAAACCCCTTTTGATTGACAGCTACAGCACGGAAGCCTAATG	3081
	2104	CCAGACATATGTGAAGGGAATTTAGAGTTTTCGAGAACTCTCTTTCTTATCCATGCGC	2163
	3082	CCGAAACACATTTGAAGSAAATGTCACATTTGTGTGAAGTTGTATTTCAACTATCCACCCGA	3141
Qy	2164	CCAGATGTTTTCATCTCTCGTGCTTATCCCTCAGTATTGACGAGSAAAGACAGTAGCA	2223
	3142	CCGGAATCCAGTCTTTCAGSACTGAGCTGGAGGTGAAGAAGGCCAGACGCTGGCT	3201
	2224	TTTGTGGGAGCAGCGGCTGTGGGAAAGACACTTCTGTTCACCTTCCTGACAGACATTAT	2283
Db	3202	CTGTTGGGACGACGTGGCTGTGGGAAGACACAGTGTGTCGAGCTCTGTGAGCGGTTCTAC	3261
	2284	GACCCGTCAGAGACAGTGTCTTTGATGTGTGATGTCGAATGCAAAAGAAATGAATGTACAG	2343
	3262	GACCCCTTGGCAGGAAGTCTCTGTGATGCAAGAAGAAATAAAGCATGTATGTTCAG	3321
Qy	2344	TGCTCTCGTTCCCAAATAGCAATCGTTTCCTCAAGAGCCTGTGCTCTTCACTTCGAGCAT	2403
	3322	TGGCTCCGAGCACACTGGGCATCTGTGTCCGAGAGCCCATCTCTTTGACTTCGAGCAT	3381
	2404	GCTTGAGAACATCCCTATGTGTGACACACAGCGTGTGTGGCTATGATGAGATCAAGAA	2463
Db	3382	GCTTGAGAACATTCCTCTATGGAGACAACGCGGGTGGTGTACAGGAAGAGATCTGTGAGG	3441
	2464	GCCGCAAAATCGACAAATATCCATCTTTTATTTGAAGGTCTCCCTGAGAAATACAAACA	2523
	3442	GCAGCAAAAGAGGCCAACATACATGCTCTTCATCGAGTCACTGCCTAATAAATATAGCACT	3501
Qy	2524	CAGTTTGGACTGAAAGAGACACAGCTTTCTGCGGCCAGAAACAAGACTAGCTATTGCA	2583
	3502	AAAGTAGGAGACAAGAGGAATCTAGCTCTCTGTGTGGCCGCAAAACACGCAATTCCTAGCT	3561
	2584	AGGGCTCTTCTCCAAAAACCCAAATTTTATTTGATGAGGCCACTTTCAGGCCCTCGAT	2643
Db	3562	CGTGCCCTTGTGTAGACAGCTCATATTTTGTCTTTTGGATGAGCCAGCTCAGCTCTGGAT	3621
	2644	AATGACAGTGAGAGGTGGTTTCAGATGCGCTTGATTAAGCCGAGGACGGGAAGGACATGC	2703
	3622	ACAGAAGTGAAAGGTTGTCCAAAGAGCCCTTGCAAGAGCCCTGCAAGAGCCAGAGNAGCGCCGCACTGC	3681

Qy	2704	CTAGTGGTCACACAGGCTCTCTGCATTCAGAACGAGATTTGATAGTGGTTCTGCAC	2763
Db	3682	ATTGTGATGTCTACCGGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGGTTTTCAG	3741
Qy	2764	AATGGAAGATAAAGGAACAAGGAACCTCATCAAGAGCTCTCTGAGAAATCGAGACATATAT	2823
Db	3742	AATGGCAGATCAGGACGATGGCAGCATCAGCAGCTGCTGGCAGAAAGGCATCTAT	3801
Qy	2824	TTTAAGTTAGTGAATGCACAGTCAG	2848
Db	3802	TTTTCAATGTCAGTGTCCAGGCTG	3826

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Job time : 1677 secs